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(21) International Application Number: <b>PCT/US94/05344</b> (22) International Filing Date: <b>12 May 1994 (12.05.94)</b> (30) Priority Data: 247620                      13 May 1993 (13.05.93)                      NZ 08/062,409                14 May 1993 (14.05.93)                      US (60) Parent Application or Grant (63) Related by Continuation US    08/062,409 (CIP) Filed on                                      14 May 1993 (14.05.93) (71)(72) Applicants and Inventors: <b>JACOBS, William, R., Jr.</b> [US/US]; 163 Fordham Street, City Island, NY 10464 (US). <b>COLLINS, Desmond, Michael</b> [NZ/NZ]; 25 Stephens Street, Upper Hutt, Wellington (NZ). <b>BANERJEE, Asesh</b> [IN/US]; Apartment B, 1935 Eastchester Road, Bronx, NY 10461 (US). <b>DE LISLE, Geoffrey, William</b> [NZ/NZ]; 41 Vista Crescent, Upper Hutt, Wellington (NZ). <b>WILSON, Theresa,</b> Mary [NZ/NZ]; 32 Karamu Crescent, Wainuiomata (NZ). (74) Agents: <b>MONROY, Gladys, M. et al.; Morrison &amp; Foerster,</b> 755 Page Mill Road, Palo Alto, CA 94304-1018 (US):	(81) Designated States: <b>AT, AU, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, ES, FI, GB, GE, HU, JP, KG, KP, KR, KZ, LK, LU, LV, MD, MG, MN, MW, NL, NO, NZ, PL, PT, RO, RU, SD, SE, SI, SK, TJ, TT, UA, US, UZ, VN, European patent (AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).</b>  Published <i>With international search report.</i>	
(54) Title: <b>METHODS AND COMPOSITIONS FOR DETECTING AND TREATING MYCOBACTERIAL INFECTIONS USING AN inhA GENE</b>  (57) Abstract  <p>The embodiments of the invention are based upon the identification and characterization of genes that determine mycobacterial resistance to the antibiotic isoniazid (INH) and its analogs. These genes, termed <i>inhA</i>, encode a polypeptide, InhA, that is the target of action of mycobacteria for isoniazid. The sequences of wild-type INH-sensitive as well as allelic or mutant INH-resistant <i>inhA</i> genes and their operons are provided. Also provided are isolated InhA polypeptides of both the INH-resistant and INH-sensitive types.</p>		

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5           METHODS AND COMPOSITIONS FOR DETECTING AND TREATING  
MYCOBACTERIAL INFECTIONS USING AN inhA GENE

10                           Statement of Government Interest

          This invention was made with government support  
under NIH Grant No. A126170 and National Cooperative Drug  
Discovery Group Grant No. U01A130189. As such, the United  
15   States government has certain rights in the invention.

CROSS-REFERENCE TO RELATED APPLICATIONS

          This is a Continuation-in-Part of Application  
Serial No. 08/062,409 filed May 14, 1993, entitled USE OF  
20   GENES OF M. TUBERCULOSIS AND M. SMEGMATIS WHICH CONFER  
ISONIAZID RESISTANCE TO TREAT TUBERCULOSIS AND TO ASSESS  
DRUG RESISTANCE.

25                           FIELD OF THE INVENTION

          The invention relates to materials and methods  
used in the diagnosis and treatment of mycobacterial  
diseases, and more specifically to DNA sequence(s)  
associated with resistance to isoniazid and its analogs in  
30   mycobacteria, methods for isolating such sequences), and  
the use of such sequence(s) in human and animal medical  
practice.

35                           BACKGROUND OF THE INVENTION

          Tuberculosis caused by members of the M.  
tuberculosis complex including M. tuberculosis, M. bovis,  
and M. africanum remains the largest cause of human death

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in the world from a single infectious disease, and is responsible for one in four avoidable adult deaths in developing countries. In addition, in 1990, there was a 10% increase in the incidence of tuberculosis in the United States. Further, M. bovis causes tuberculosis in a wide range of animals, and is a major cause of animal suffering and economic loss in animal industries.

Infection with drug-sensitive strains of the M. tuberculosis complex can be effectively cured with a combination of antibiotics, including isoniazid (isonicotinic acid hydrazide, INH), rifampicin, and pyrazinamide. INH was first reported to be active against M. tuberculosis in 1952, and particularly active against M. tuberculosis and M. bovis. However, mutants resistant to INH have emerged since then, and today such mutants account for as many as 26% of the clinical M. tuberculosis isolates in certain U.S. cities.

Some INH-resistant strains are associated with a loss of catalase activity, and deletions of the catalase-peroxidase gene (katG) correlate with INH resistance in certain M. tuberculosis isolates. Furthermore, transfer of the wild-type (wt) M. tuberculosis katG gene to INH-resistant M. smegmatis and M. tuberculosis confers INH sensitivity, suggesting that catalase-peroxidase activity is required for INH-sensitivity. However, in some studies only 10 to 25% of the INH-resistant isolates appear to be catalase negative, indicating that INH resistance can be due to other factors.

Drug resistance can be caused by many mechanisms, including mutations in the drug target that reduce the binding of the drug or mutations that lead to increased production of the target. The mechanism by which INH inhibits mycobacteria and its precise target of action are unknown. Biochemical evidence has suggested that both INH and ethionamide (ETH, a structural analog of INH) block

mycolic acid biosynthesis in mycobacteria. INH has been found to inhibit mycolic acid biosynthesis in cell-free extracts of mycobacteria, but the target protein has not been identified. In addition, in certain cases, low-level  
5 INH resistance correlates not with the loss of catalase activity but with the coacquisition of ETH resistance, suggesting that the two drugs may share a common target.

Because such a high percentage of the M. tuberculosis complex strains are resistant to INH, a great  
10 need exists to identify its targets of action, and thereby to devise rapid methods for identification of INH-resistant strains and methods of treating individuals for prevention and/or treatment of the disease associated with them.

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#### SUMMARY OF THE INVENTION

This invention is based upon the discovery of a gene, inhA (also called ps5), that encodes an enzyme (InhA). InhA is the target of action of isoniazid in  
20 mycobacteria. Mutations within the inhA gene result in isoniazid resistance. Thus, the present invention provides isolated and recombinant polynucleotide sequences and polypeptides encoded therein that are associated with resistance to INH and its structural analogs in members of  
25 the genus mycobacteria, particularly those of the M. tuberculosis complex, including M. tuberculosis, M. africanum and M. bovis; the M. avium complex, including M. avium, M. intracellulare, M. scrofulaceum, and M. paratuberculosis; M. smegmatis. It also provides the  
30 allelic counterparts that are associated with INH sensitivity. The polynucleotides of the invention have many uses. For example, they are useful in assessing the susceptibility of various strains of the M. tuberculosis  
35 complex to isoniazid type antibiotics, as decoys and antisense oligonucleotides to prevent the expression of

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polypeptides associated with isoniazid resistance, and for the expression of the polypeptides encoded therein. The polypeptides encoded in the polynucleotides and/or antibodies directed to them may also have use in immunoassays for the detection of INH-resistant strains, in the determination of whether an INH-type antibiotic may be effective against tuberculosis, and in the treatment of individuals for infection with these strains.

Accordingly, embodiments of the invention include the following.

An isolated wild-type gene which encodes an enzyme which is the target of action for isoniazid.

An isolated wild-type gene which encodes a polypeptide (InhA) which is the target of action for isoniazid (INH). These wild type genes also include those from M. tuberculosis, M. avium, M. smegmatis, and M. bovis.

An isolated mutant gene that encodes InhA wherein the mutant gene is associated with INH-resistance.

An isolated polynucleotide encoding an InhA polypeptide or fragment or variant thereof. These polynucleotides include recombinant expression vectors comprised of control sequences operably linked to a segment encoding the InhA polypeptide or fragment or variant thereof.

A host cell comprised of any of the aforementioned polynucleotides.

A method of treating an individual for infection caused by a member of the mycobacterial complex comprising:

(a) providing a composition comprised of a polynucleotide capable of inhibiting mRNA activity from an inhA operon of the infecting species and a suitable excipient; and

(b) administering a pharmacologically effective amount of said composition to the individual.

The above-mentioned method wherein the mode of

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administration of the polynucleotides is oral, enteral, subcutaneous, intraperitoneal or intravenous.

A method of assessing susceptibility of a strain of mycobacteria in a biological sample to INH comprising:

- 5           (a) providing the mycobacterial DNA from the biological sample;
- (b) amplifying a region of the inhA operon;
- (c) determining whether a mutation exists within the inhA operon from the biological sample, the presence of
- 10   the mutation indicating that said mycobacterial strain is resistant to INH.

The aforementioned method of wherein the amplification is by a polymerase chain reaction (PCR).

- In addition, the aforementioned method further
- 15   comprised of providing a comparable portion of wild-type INH-sensitive inhA operon from the mycobacteria, and the determination of whether a mutation exists in the biological sample is by comparison with the wild-type inhA operon.

- 20           The aforementioned method wherein determining whether a mutation exists is performed by single strand conformation polymorphism analysis.

A method of determining whether a drug is effective against mycobacterial infection comprising:

- 25           (a) providing isolated InhA;
- (b) providing a candidate drug;
- (c) mixing InhA with substrates for mycolic acid biosynthesis in the presence or absence of the candidate drug; and
- 30           (d) measuring the inhibition of biosynthesis of mycolic acid caused by the presence of the drug, if any.

- A method of producing a tuberculosis-specific mycolic acid comprising adding purified InhA to substrates required for the biosynthesis of mycolic acid.
- 35

A method for producing a compound that inhibits

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InhA activity comprising:

- a. providing purified InhA;
- b. determining the molecular structure of said InhA;
- 5 c. creating a compound with a similar molecular structure to INH; and
- d. determining that said compound inhibits the biochemical activity of InhA.

10 An isolated InhA polypeptide or fragment or variant thereof.

A recombinant mycobacterial vaccine comprised of attenuated mutants selected from the group consisting of BCG, M. tuberculosis, and M. bovis, wherein the mutants are host cells containing a mutated inhA gene.

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#### BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 is a table listing inhA genes from different mycobacteria that confer resistance to INH and ETH in M. smegmatis mc<sup>2</sup> 155.

20

Figure 2, comprised of sheets 2A through 2F, presents a comparison of the coding strands of DNA sequences from M. bovis that confer resistance to INH and from M. tuberculosis and M. smegmatis that confer sensitivity to INH. The mutation in mc<sup>2</sup>651 that causes INH-resistance is indicated by the arrow.

25

Figure 3 is a diagram of the subcloning strategy used to demonstrate that the isoniazid resistance phenotype is conferred by the inhA open reading frame.

30

Figure 4, comprised of sheets 4A and 4B, shows the alignment of the amino acid sequences of InhA proteins from M. tuberculosis H37R, M. bovis, M. bovis NZ, M. smegmatis mc<sup>2</sup>155 and M. smegmatis mc<sup>2</sup>651 with EnvM proteins from S. typhimurium and E. coli.

35

Figure 5 is a bar graph showing the results of cell-free assays of mycolic acid biosynthesis, and the effect of insertion of inhA genes on the effect of INH.

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Figure 6 is a diagram of the allelic exchange experiment demonstrating that the point mutation in the mc<sup>2</sup>651 inhA polynucleotide results in INH-resistance, and the results obtained from the experiment.

Figure 7, comprised of sheets 7A-1 through 7A-2, 7B-1 through 7B-3, and 7C-1 through 7C-2, shows the nucleic acid sequence that includes the M. smegmatis inhA gene.

Figure 8, comprised of sheets 8A, 8B, and 8C, shows the nucleic acid sequence that includes the M. tuberculosis inhA gene.

Figure 9, comprised of sheets 9A, 9B, 9C and 9D, shows the nucleic acid sequence for pS5 and the amino acid sequence from two large open reading frames encompassed within it.

Figure 10 presents the amino acid sequence of a fragment encoded by nucleic acid residues 1256-2062 (ORF2) of the pS5 operon.

Figure 11 presents the amino acid sequence encoded by nucleic acid residues 494-1234 (ORF1) of the pS5 operon.

Figure 12, comprised of sheets 12A through 12C, presents the amino acid sequence of the M. bovis pS5 operon.

Figure 13 presents a restriction enzyme map of pYUB18 showing some significant features of the genome.

#### DETAILED DESCRIPTION OF THE INVENTION

The invention stems from the discovery of inhA, a gene that encodes a polypeptide that is a target for INH and ETH in members of the M. tuberculosis complex. Mutations of the gene render mycobacteria INH- and ETH-resistant. The gene and mutations within it were identified using a genetic strategy. Genomic libraries were constructed in shuttle cosmid vectors from INH-

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resistant mutants of M. smegmatis and M. bovis. Transferral of the libraries into wild type (i.e., INH-sensitive) M. smegmatis strains allowed the identification of clones that consistently conferred INH-resistance (shown in the table in Figure 1). The transformation of cosmids containing a cross-hybridizing DNA fragment from wt (INH-ETH-sensitive strains of M. smegmatis, M. tuberculosis, M. bovis, M. bovis BCG, and M. avium yielded clones that conferred INH-ETH resistance. These results were suggestive that overexpression of a putative target gene, inhA, on a multi-copy plasmid conferred an INH-resistance phenotype. This led to the conclusion that InhA, the gene product of inhA, is the target of action for INH in members of the M. tuberculosis complex. Moreover, the results showing that a 3 kb BamHI DNA fragment from the M. smegmatis cosmid that conferred INH-resistance strongly hybridized to all of eleven mycobacterial species tested demonstrated that the inhA gene is highly conserved among mycobacteria.

The DNA fragments that conferred INH-sensitivity to M. smegmatis and M. tuberculosis, as well as those that were isolated from mutant INH-resistant M. smegmatis and M. bovis strains were subjected to DNA sequencing. These DNA sequences are shown in Figure 2. Figure 2 presents the DNA sequences of the INH-resistant polynucleotide from M. bovis and the INH-sensitive polynucleotides of M. tuberculosis and M. smegmatis. Sequence analysis revealed two ORFs, encoding proteins of 29 and 32 kD. Subcloning analyses of the M. smegmatis fragment demonstrated that the ORF encoding the 29 kD protein was responsible for the INH-resistance phenotype, and was termed the inhA gene. In the M. bovis and M. tuberculosis genomes, it appears that the inhA genes are positioned such that they are subject to the same transcriptional control elements (including the promoter) as is ORF1, whereas the inhA gene has its own

promoter in the M. smegmatis genome.

The M. tuberculosis and M. smegmatis inhA gene products show 38 and 40% homologies to the envM gene product of S. typhimurium. In addition, in the M. smegmatis, M. tuberculosis, and M. bovis genomes the inhA ORFs are preceded by another ORF that shares 40% identity with acetyl CoA reductases. The similarities of the inhA ORF and ORF1 to lipid biosynthetic genes are consistent with the hypothesis that INH inhibits an enzyme involved in mycolic acid biosynthesis.

Sequence analysis and comparison of inhA from the mutant INH-resistant and wt INH-sensitive strains of M. smegmatis (See Figure 4) and M. bovis revealed the presence of a single base pair difference that resulted in the amino acid substitution of an alanine for a serine at position 94 of the InhA protein. (See Figure 4.) As shown in the Examples, this difference caused the Inh-resistance phenotype.

Polynucleotides from M. smegmatis, M. tuberculosis, and M. bovis that encode InhA have been identified, isolated, cloned, sequenced and characterized. The nucleic acid sequences for these polynucleotides are shown in Figures 7, 8, and 9 respectively. Figure 9 also shows the amino acids encoded in the polynucleotide.

A comparison of the sequences for M. tuberculosis inhA and M. bovis inhA shows that the inhA gene from INH-sensitive M. tuberculosis and INH-sensitive M. bovis are identical. Given that the mutation of Ser to Ala conferring INH-resistance is conserved in M. smegmatis and M. bovis phenotypes, it can be anticipated that other INH-resistant isolates will be found that are due to mutations in the inhA operon. For example, INH-resistance may also be due to missense mutations in the coding region of inh, or to mutations that cause the overexpression of InhA (e.g., mutations in the regulatory regions of the operon,

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and/or duplications that allow overexpression).

The discovery of inhA genes and operons of the mycobacterial complex that confer INH-resistance allows for the preparation and use of compositions and methods useful in the diagnosis and treatment of pathogenic states resulting from infection with these microorganisms, and particularly with INH-resistant strains.

The practice of the present invention will employ, unless otherwise indicated, conventional techniques of molecular biology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature. See e.g., Sambrook, Fritsch, and Maniatis, MOLECULAR CLONING: A LABORATORY MANUAL, Second Edition (1989), OLIGONUCLEOTIDE SYNTHESIS (M.J. Gait Ed., 1984), the series METHODS IN ENZYMOLOGY (Academic Press, Inc.); GENE TRANSFER VECTORS FOR MAMMALIAN CELLS (J.M. Miller and M.P. Calos eds. 1987), HANDBOOK OF EXPERIMENTAL IMMUNOLOGY, (D.M. Weir and C.C. Blackwell, Eds.), CURRENT PROTOCOLS IN MOLECULAR BIOLOGY (F.M. Ausubel, R. Brent, R.E. Kingston, D.D. Moore, J.G. Siedman, J.A. Smith, and K. Struhl, eds., 1987), and CURRENT PROTOCOLS IN IMMUNOLOGY (J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach and W. Strober, eds., 1991).

As used herein the term "target of action for isoniazid" refers to a polypeptide, InhA, encoded in an inhA operon of mycobacteria, and preferably in members of the mycobacterial complex.

As used herein, the term "inhA gene" refers to a polynucleotide that encodes a polypeptide that is present in mycobacteria, wherein the polypeptide has substantial amino acid homology and equivalent function to the InhA proteins of M. tuberculosis, M. bovis, or M. smegmatis; amino acid sequences of variants of these InhA proteins are shown in Figure 4. In this context substantial amino acid

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homology means at least about 60% homology, generally at least about 70% homology, even more generally at least about 80% homology, and at times at least about 90% homology to any of the indicated polypeptides.

5           As used herein the term "polynucleotide" refers to a polymeric form of nucleotides of any length, either ribonucleotides or deoxyribonucleotides. This term refers only to the primary structure of the molecule. Thus, this term includes double- and single-stranded DNA and RNA. It  
10 also includes known types of modifications, for example, labels which are known in the art (e.g., Sambrook, et al.), methylation, "caps", substitution of one or more of the naturally occurring nucleotides with an analog, internucleotide modifications such as, for example, those  
15 with uncharged linkages (e.g., methyl phosphonates, phosphotriesters, phosphoamidates, carbamates, etc.), those containing pendant moieties, such as, for example, proteins (including for e.g., nucleases, toxins, antibodies, signal peptides, poly-L-lysine, etc.), those with intercalators  
20 (e.g., acridine, psoralen, etc.), those containing chelators (e.g., metals, radioactive metals, boron, oxidative metals, etc.), those containing alkylators, those with modified linkages (e.g., alpha anomeric nucleic acids, etc.), as well as unmodified forms of the polynucleotide.

25           The invention includes as an embodiment an isolated polynucleotide comprised of a sequence encoding a polypeptide associated with isoniazid (INH) resistance in mycobacteria or active fragment thereof. These isolated polynucleotides contain less than about 50%, preferably  
30 less than about 70%, and more preferably less than about 90% of the chromosomal genetic material with which the sequence encoding the polypeptide is usually associated in nature. An isolated polynucleotide "consisting essentially of"  
35 a sequence encoding an isoniazid resistance associated polypeptide lacks other sequences encoding other

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polypeptides derived from the mycobacterial chromosome.

As used herein "isoniazid" ("INH") refers to isoniazid and analogs thereof that inhibit mycobacterial replication by inhibiting the activity of the same  
5 polypeptide(s) INH inhibits, for example, ethonamide (ETH).

The invention also includes as embodiments recombinant polynucleotides containing a region encoding inhA gene products for mycobacteria. The term "recombinant polynucleotide" as used herein intends a polynucleotide of  
10 genomic, cDNA, semisynthetic, or synthetic origin which, by virtue of its origin or manipulation: (1) is not associated with all or a portion of a polynucleotide with which it is associated in nature; or (2) is linked to a polynucleotide other than that to which it is linked in nature; or (3)  
15 does not occur in nature.

A purified or recombinant polynucleotide comprised of a sequence encoding InhA of mycobacteria or variant or active fragment thereof, may be prepared by any technique known to those of skill in the art using the  
20 polynucleotide sequences provided herein. For example, they can be prepared by isolating the polynucleotides from a natural source, or by chemical synthesis, or by synthesis using recombinant DNA techniques.

It is contemplated that the sequence encoding an  
25 InhA encodes a polypeptide that is associated with isoniazid resistance or sensitivity in mycobacteria, and that allelic variations of the sequences, some of which are shown in the Figures are contemplated herein. The term "polypeptide" refers to a polymer of amino acids and does  
30 not refer to a specific length of the product; thus, peptides, oligopeptides, and proteins are included within the definition of polypeptide. This term also does not refer to or exclude post-expression modifications of the  
35 polypeptide, for example, glycosylations, acetylations, phosphorylations and the like. Included within the

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definition are, for example, polypeptides containing one or more analogs of an amino acid (including, for example, unnatural amino acids, etc.), polypeptides with substituted linkages, as well as the modifications known in the art, both naturally occurring and non-naturally occurring.

Also contemplated within the invention are cloning vectors and expression vectors comprised of a sequence encoding *InhA* or variant or fragment thereof. Suitable cloning vectors may be constructed according to standard techniques, or may be selected from the large number of cloning vectors available in the art. While the cloning vector selected may vary according to the host cell intended to be used, useful cloning vectors will generally have the ability to self replicate, may possess a single target for a restriction endonuclease, and may carry genes for a readily selectable marker (e.g., antibiotic resistance or sensitivity markers). Suitable examples include plasmids and bacterial viruses, e.g., PUC18, mp18, mp19, PBR322, pMB9, Cole1, pCR1, RP4, phage DNAs, and shuttle vectors (e.g., pSA3 and pAT28. Preferred vectors include pBluescript IIks (Stratagene), and pYUB18.

Expression vectors generally are replicable polynucleotide constructs that encode a polypeptide operably linked to suitable transcriptional and translational regulatory elements. Examples of regulatory elements usually included in expression vectors are promoters, enhancers, ribosomal binding sites, and transcription and translation initiation and termination sequences. The regulatory elements employed in the expression vectors containing a polynucleotide encoding *InhA* or an active fragment would be functional in the host cell used for expression. It is also contemplated that the regulatory sequences may be derived from the *inhA* operon; thus, a promoter or terminator sequence may be homologous (i.e., from mycobacteria) to the coding sequence.

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The invention also includes recombinant host cells comprised of any of the above described polynucleotides that contain a sequence encoding an InhA polypeptide of mycobacteria. The polynucleotides may be inserted into the host cell by any means known in the art. As used herein, "recombinant host cells", "host cells", "cells", "cell lines", "cell cultures", and other such terms denoting microorganisms or higher eukaryotic cell lines cultured as unicellular entities refer to cells which can be, or have been, used as recipients for recombinant vector or other transfer DNA, and include the progeny of the original cell which has been transformed. It is understood that the progeny of a single parental cell may not necessarily be completely identical in morphology or in genomic or total DNA complement as the original parent, due to natural, accidental, or deliberate mutation. Hosts which may be used include prokaryotic cells (e.g., bacterial cells such as E. coli, mycobacteria, and the like) and eukaryotic cells (e.g., fungal cells, insect cells, animal cells, and plant cells, and the like). Prokaryotic cells are generally preferred, and E. coli and M. smegmatis are particularly suitable. Of the latter, mc<sup>2</sup>155 is particularly preferred.

"Transformation", as used herein, refers to the insertion of an exogenous polynucleotide into a host cell, irrespective of the method used for the insertion, for example, direct uptake, transduction, f-mating or electroporation. The exogenous polynucleotide may be maintained as a non-integrated vector, for example, a plasmid, or alternatively, may be integrated into the host cell genome.

The polynucleotides comprised of sequences encoding InhA are of use in the detection of INH-resistant forms of mycobacteria in biological samples. As used herein, a "biological sample" refers to a sample of tissue



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labelled, for example with radioactive isotopes. Usual isotopes include, for example  $^{32}\text{P}$  and  $^{33}\text{P}$ . The probes are capable of hybridizing to the genetic elements associated with INH-resistance. Preferably, the probes are specific  
5 for sequences that encode the INH-resistance gene. By way of example, the probe may be the entire nucleotide sequence depicted in Figure 12. However, shorter probes are preferred.

For use of such probes as diagnostics, the biological sample to be analyzed, such as blood or serum, may  
10 be treated, if desired, to extract the nucleic acids contained therein. The resulting nucleic acid from the sample may be subjected to gel electrophoresis or other size separation techniques; alternatively, the nucleic acid  
15 sample may be dot blotted without size separation. The probes are usually labeled. Suitable labels, and methods for labeling probes are known in the art, and include, for example, radioactive labels incorporated by nick translation or kinasing, biotin, fluorescent probes, and  
20 chemiluminescent probes. The nucleic acids extracted from the sample are then treated with the labeled probe under hybridization conditions of suitable stringencies. The probes can be made completely complementary to the allelic form of polynucleotide that has been targeted. With this  
25 goal, high stringency conditions usually are desirable in order to prevent false positives. The stringency of hybridization is determined by a number of factors during hybridization and during the washing procedure, including temperature, ionic strength, length of time, and  
30 concentration of formamide. These factors are outlined in, for example, Maniatis, T. (1982).

It may be desirable to use amplification techniques in hybridization assays. Such techniques are  
35 known in the art and include, for example, the polymerase chain reaction (PCR) technique described which is by Saiki

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or fluid isolated from an individual, including but not limited to, for example, plasma, serum, spinal fluid, lymph fluid, the external sections of the skin, respiratory, intestinal, and genitourinary tracts, tears, saliva, milk, blood cells, tumors, organs, and also samples of in vitro cell culture constituents (including but not limited to conditioned medium resulting from the growth of cells in cell culture medium, putatively infected cells, recombinant cells, and cell components). As used herein, the term "clinical sample" is synonymous with "biological sample".

The term "individual" as used herein refers to vertebrates, particularly members of the mammalian or avian species, and includes but is not limited to domestic animals, sports animals, and primates, including humans.

Using the disclosed portions of the isolated polynucleotides encoding InhA as a basis, oligomers of approximately 8 nucleotides or more can be prepared, either by excision from recombinant polynucleotides or synthetically, which hybridize with the mycobacterial sequences in the plasmids and are useful in identification of the INH-resistant and INH-sensitive mycobacteria. The probes are a length which allows the detection of the InhA encoding sequences by hybridization. While 6-8 nucleotides may be a workable length, sequences of 10-12 nucleotides are preferred, and about 20 nucleotides appears optimal. These probes can be prepared using routine methods, including automated oligonucleotide synthetic methods. For use as probes, complete complementarity is desirable, though it may be unnecessary as the length of the fragment is increased.

Thus, a polynucleotide comprising all or part of the nucleic acid sequences of an inhA operon, and particularly an inhA gene may be used as probes for identifying nucleic acids which code for polynucleotides associated with INH-resistance. The probes may be

et al. (1986), by Mullis, U.S. Patent No. 4,683,195, and by Mullis et al. U.S. Patent No. 4,683,202. This technique may be used in conjunction with other techniques, for example, in single-strand conformation polymorphism analysis (see infra., in the Examples).

The probes can be packaged into diagnostic kits. Diagnostic kits include the probe DNA, which may be labeled; alternatively, the probe DNA may be unlabeled and the ingredients for labeling may be included in the kit in separate containers. The kit may also contain other suitably packaged reagents and materials needed for the particular hybridization protocol, for example, standards, as well as instructions for conducting the test. If the kit is to be used for an assay system which includes PCR technology it may also include primers for the PCR reaction.

The inhA gene sequence and polypeptides encoded therein may also be used for screening for drugs against mycobacteria, particularly members of the mycobacterial complex, and more particularly M. tuberculosis and M. bovis. For example, it can be used to express the INH-resistant and INH-sensitive polypeptides encoded in the allelic forms of inhA. Utilizing these polypeptides in vitro assays, one could monitor the effect of candidate drugs on mycolic acid biosynthesis. Drugs that inhibit mycolic acid biosynthesis are candidates for therapy of mycobacterial diseases. Drugs that may be tested for effectiveness in this type of system include INH, ETH, rifampicin, streptomycin, ethambutol, ciprofloxacin, novobiocin and cyanide.

The inhA operon sequences may also be used to design polynucleotides that can be used for treatment of mycobacterial infections, including those caused by M. tuberculosis, M. avium, M. smegmatis, and M. bovis. One method of treating a mycobacterial infection utilizing the

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InhA gene is by providing antisense polynucleotides or triplex forming polynucleotides which can be used to inhibit the transcription or translation of mRNA from the inhA operon, for example antisense polynucleotides, triplex forming polynucleotides, decoys, and ribozymes. Thus, these types of polynucleotides are also included within the invention. These polynucleotides may be prepared by a variety of techniques known in the art, including chemical synthesis and recombinant technology. After preparation they can then be administered, either alone or in combination with other compositions to treat mycobacterial infections, including tuberculosis. The compositions containing these polynucleotides may also include suitable excipients.

The sequence of inhA can also be used to assess the susceptibility of various strains of mycobacteria, and particularly of M. tuberculosis or M. bovis, in a clinical sample to INH. This susceptibility comparison is based upon the detection of a mutant allele as compared to the wild-type inhA allele that is INH-sensitive. Procedures to perform this type of assessment will be readily evident to those of skill in the art. For example, one procedure to perform this assessment is described in the Examples, and is based upon isolation of the chromosomal DNA of the bacterium, amplification of the inhA region by PCR using primers specific for the region (based upon the inhA sequences provided herein, and determination whether a mutation exists in the isolated DNA by the method of single strand conformation polymorphism analysis.

In addition, compounds which block the activity of InhA polypeptides (which may be enzymes) can be prepared utilizing the sequence information of inhA. This is performed by overexpressing InhA, purifying the polypeptide, and then performing X-ray crystallography on the purified InhA polypeptide to obtain its molecular

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structure. Next, compounds are created which have similar molecular structures to all or portions of the polypeptide. The compounds are then combined with the polypeptide and attached thereto so as to block the biochemical activity of the InhA polypeptide.

The inhA polynucleotides may also be used to produce or improve live attenuated or killed tuberculosis vaccines. For example, a tuberculosis strain which contains a mutated inhA can be administered in vaccine form to eliminate INH-resistance which is typically conferred by mutant inhA. In addition, mutated inhA genes may be added to BCG or M. tuberculosis vaccines to provide attenuated mutant tuberculosis vaccines. These vaccines may be used to treat and prevent a wide variety of diseases, including tuberculosis, AIDS, leprosy, polio, malaria and tetanus.

The polypeptides of the invention include those encoded in allelic variants of inhA, some of which are shown in the Figures herein, and are in purified or recombinant form. These polypeptides include fragments of the entire polypeptides encoded in the ORFs, particularly fragments that exhibit activity in mycolic acid biosynthesis. In addition, polypeptides of the invention include variants of InhA which differ from the native amino acid sequences by the insertion, substitution, or deletion of one or more amino acids. These variants may be prepared chemically, or by alteration of the polynucleotide sequence encoding InhA, using techniques known in the art, for example, by site-specific primer directed mutagenesis. These polypeptides can be purified by any means known in the art, including, for example freeze-thaw extraction, salt fractionation, column chromatography, affinity chromatography and the like.

The polypeptides of the invention may find use as therapeutic agents for treatment of mycobacterial infection. "Treatment" as used herein refers to

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prophylaxis and/or therapy.

The InhA polypeptides can be prepared as discrete entities or incorporated into a larger polypeptide, and may find use as described herein. The immunogenicity of the epitopes of InhA may also be enhanced by preparing them in mammalian or yeast systems fused with or assembled with particle-forming proteins such as, for example, that associated with hepatitis B surface antigen. See, e.g., U.S. Pat. No. 4,722,840. Vaccines may be prepared from one or more immunogenic polypeptides derived from InhA.

The preparation of vaccines which contain an immunogenic polypeptide(s) as active ingredients, is known to one skilled in the art. Typically, such vaccines are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid prior to injection may also be prepared. The preparation may also be emulsified, or the protein encapsulated in liposomes. The active immunogenic ingredients are often mixed with excipients which are pharmaceutically acceptable and compatible with the active ingredient. Suitable excipients are, for example, water, saline, dextrose, glycerol, ethanol, or the like and combinations thereof. In addition, if desired, the vaccine may contain minor amounts of auxiliary substances such as wetting or emulsifying agents, pH buffering agents, and/or adjuvants which enhance the effectiveness of the vaccine. Examples of adjuvants which may be effective include but are not limited to: aluminum hydroxide, N-acetyl-muramyl-L-threonyl-D-isoglutamine (thr-MDP), N-acetyl-nor-muramyl-L-alanyl-D-isoglutamine (CGP 11637, referred to as nor-MDP), N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'-2'-dipalmitoyl-sn-glycero-3-hydroxyphosphoryloxy)-ethylamine (CGP 19835A, referred to as MTP-PE), and RIBI, which contains three components extracted from bacteria,

monophosphoryl lipid A, trehalose dimycolate and cell wall skeleton (MPL+TDM+CWS) in a 2% squalene/Tween 80 emulsion. The effectiveness of an adjuvant may be determined by measuring the amount of antibodies directed against an immunogenic polypeptide containing an InhA antigenic sequence resulting from administration of this polypeptide in vaccines which are also comprised of the various adjuvants.

The vaccines are conventionally administered parenterally, by injection, for example, either subcutaneously or intramuscularly. Additional formulations which are suitable for other modes of administration include suppositories and, in some cases, oral formulations or formulations suitable for distribution as aerosols. For suppositories, traditional binders and carriers may include, for example, polyalkylene glycols or triglycerides; such suppositories may be formed from mixtures containing the active ingredient in the range of 0.5% to 10%, preferably 1%-2%. Oral formulations include such normally employed excipients as, for example, pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharine, cellulose, magnesium carbonate, and the like. These compositions take the form of solutions, suspensions, tablets, pills, capsules, sustained release formulations or powders and contain 10%-95% of active ingredient, preferably 25%-70%.

The proteins may be formulated into the vaccine as neutral or salt forms. Pharmaceutically acceptable salts include the acid addition salts (formed with free amino groups of the peptide) and which are formed with inorganic acids such as, for example, hydrochloric or phosphoric acids, or such organic acids such as acetic, oxalic, tartaric, maleic, and the like. Salts formed with the free carboxyl groups may also be derived from inorganic bases such as, for example, sodium, potassium, ammonium,

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calcium, or ferric hydroxides, and such organic bases as isopropylamine, trimethylamine, 2-ethylamino ethanol, histidine, procaine, and the like.

5       The vaccines are administered in a manner compatible with the dosage formulation, and in such amount as will be prophylactically and/or therapeutically effective. The quantity to be administered, which is generally in the range of 5 micrograms to 250 micrograms of antigen per dose, depends on the subject to be treated, capacity of  
10   the subject's immune system to synthesize antibodies, and the degree of protection desired. Precise amounts of active ingredient required to be administered may depend on the judgment of the practitioner and may be peculiar to each subject.

15       The vaccine may be given in a single dose schedule, or preferably in a multiple dose schedule. A multiple dose schedule is one in which a primary course of vaccination may be with 1-10 separate doses, followed by other doses given at subsequent time intervals required to  
20   maintain and or reenforce the immune response, for example, at 1-4 months for a second dose, and if needed, a subsequent dose(s) after several months. The dosage regimen will also, at least in part, be determined by the need of the individual and be dependent upon the judgment  
25   of the practitioner.

In addition, the vaccine containing the immunogenic InhA antigen(s) may be administered in conjunction with other immunoregulatory agents, for example, immune globulins, as well as antibiotics.

30       The InhA antigens may be used for the preparation of antibodies. The immunogenic polypeptides prepared as described above are used to produce antibodies, including polyclonal and monoclonal. If polyclonal antibodies are  
35   desired, a selected mammal (e.g., mouse, rabbit, goat, horse, etc.) is immunized with an immunogenic polypeptide



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bearing an InhA epitope(s). Serum from the immunized animal is collected and treated according to known procedures. If serum containing polyclonal antibodies to an InhA epitope contains antibodies to other antigens, the polyclonal antibodies can be purified by immunoaffinity chromatography. Techniques for producing and processing polyclonal antisera are known in the art, see for example, Mayer and Walker (1987).

Monoclonal antibodies directed against InhA epitopes can also be readily produced by one skilled in the art. The general methodology for making monoclonal antibodies by hybridomas is well known. Immortal antibody-producing cell lines can be created by cell fusion, and also by other techniques such as direct transformation of B lymphocytes with oncogenic DNA, or transfection with Epstein-Barr virus. See, e.g., M. Schreier et al. (1980); Hammerling et al. (1981); Kennett et al. (1980); see also, U.S. Patent Nos. 4,341,761; 4,399,121; 4,427,783; 4,444,887; 4,466,917; 4,472,500; 4,491,632; and 4,493,890. Panels of monoclonal antibodies produced against InhA epitopes can be screened for various properties; i.e., for isotype, epitope affinity, etc.

Antibodies, both monoclonal and polyclonal, which are directed against InhA epitopes are particularly useful in diagnosis, and those which are neutralizing may be useful in passive immunotherapy. Monoclonal antibodies, in particular, may be used to raise anti-idiotypic antibodies.

Anti-idiotypic antibodies are immunoglobulins which carry an "internal image" of the antigen of the infectious agent against which protection is desired. See, for example, Nisonoff, A., et al. (1981) and Dreesman et al. (1985). Techniques for raising anti-idiotypic antibodies are known in the art. See, for example, Grzych (1985), MacNamara et al. (1984), and Uytdehaag et al. (1985). These anti-idiotypic antibodies may also be useful

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for treatment, vaccination and/or diagnosis of mycobacterial infections, as well as for an elucidation of the immunogenic regions of InhA antigens.

Both the InhA polypeptides and anti-InhA antibodies are useful in immunoassays to detect presence of antibodies to mycobacteria, or the presence of the InhA antigens, and particularly the presence of INH-resistant InhA in biological samples. Design of the immunoassays is subject to a great deal of variation, and many formats are known in the art. The immunoassay will utilize at least one epitope derived from InhA. In one embodiment, the immunoassay uses a combination of epitopes derived from InhA. These epitopes may be derived from the same or from different bacterial polypeptides, and may be in separate recombinant or natural polypeptides, or together in the same recombinant polypeptides. An immunoassay may use, for example, a monoclonal antibody directed towards an InhA epitope(s), a combination of monoclonal antibodies directed towards epitopes of one mycobacterial antigen, monoclonal antibodies directed towards epitopes of different mycobacterial antigens, polyclonal antibodies directed towards the same antigen, or polyclonal antibodies directed towards different antigens. Protocols may be based, for example, upon competition, or direct reaction, or sandwich type assays. Protocols may also, for example, use solid supports, or may be by immunoprecipitation. Most assays involve the use of labeled antibody or polypeptide; the labels may be, for example, enzymatic, fluorescent, chemiluminescent, radioactive, or dye molecules. Assays which amplify the signals from the probe are also known; examples of which are assays which utilize biotin and avidin, and enzyme-labeled and mediated immunoassays, such as ELISA assays.

Typically, an immunoassay for an anti-InhA antibody(s) will involve selecting and preparing the test

sample suspected of containing the antibodies, such as a biological sample, then incubating it with an antigenic (i.e., epitope-containing) InhA polypeptide(s) under conditions that allow antigen-antibody complexes to form, and then detecting the formation of such complexes. Suitable incubation conditions are well known in the art. The immunoassay may be, without limitations, in a heterogenous or in a homogeneous format, and of a standard or competitive type.

In a heterogeneous format, the polypeptide is typically bound to a solid support to facilitate separation of the sample from the polypeptide after incubation. Examples of solid supports that can be used are nitrocellulose (e.g., in membrane or microtiter well form), polyvinyl chloride (e.g., in sheets or microtiter wells), polystyrene latex (e.g., in beads or microtiter plates, polyvinylidene fluoride (known as Immulon), diazotized paper, nylon membranes, activated beads, and Protein A beads. For example, Dynatech Immulon <sup>1</sup> or Immulon <sup>2</sup> microtiter plates or 0.25 inch polystyrene beads (Precision Plastic Ball) can be used in the heterogeneous format. The solid support containing the antigenic polypeptide is typically washed after separating it from the test sample, and prior to detection of bound antibodies. Both standard and competitive formats are known in the art.

Complexes formed comprising anti-InhA antibody (or, in the case of competitive assays, the amount of competing antibody) are detected by any of a number of known techniques, depending on the format. For example, unlabeled anti-InhA antibodies in the complex may be detected using a conjugate of antixenogeneic Ig complexed with a label, (e.g., an enzyme label).

In immunoassays where InhA polypeptides are the analyte, the test sample, typically a biological sample, is incubated with anti-InhA antibodies under conditions that

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allow the formation of antigen-antibody complexes. It may be desirable to treat the biological sample to release putative bacterial components prior to testing. Various formats can be employed. For example, a "sandwich assay" may be employed, where antibody bound to a solid support is incubated with the test sample; washed; incubated with a second, labeled antibody to the analyte, and the support is washed again. Analyte is detected by determining if the second antibody is bound to the support. In a competitive format, which can be either heterogeneous or homogeneous, a test sample is usually incubated with antibody and a labeled, competing antigen is also incubated, either sequentially or simultaneously. These and other formats are well known in the art.

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The following examples are provided only for illustrative purposes, and not to limit the scope of the present invention. In light of the present disclosure numerous embodiments within the scope of the claims will be apparent to those of ordinary skill in the art.

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### EXAMPLES

#### Example 1

#### Selection of INH-Resistant *M. bovis* Strains

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In order to select *M. bovis* INH-resistant strains, a virulent wild-type New Zealand strain of *M. bovis* was cloned by four serial passages using a combination of liquid Tween albumin broth (TAB) and 7H10 pyruvate agar culture media. A single colony of *M. bovis* was inoculated into TAB and incubated until visible growth was apparent. An appropriate dilution of the bacterial suspension in TAB was plated onto the agar media to obtain discrete colonies. After incubation, a single colony was picked and inoculated into TAB and the cloning procedure

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was repeated. After four cloning cycles a G4 strain was obtained. INH-resistant strains were obtained by growing the GI strain in liquid TAB media containing differing concentrations of INH. After incubation, the strain that  
5 had luxuriant growth in the highest concentration of INH was inoculated onto INH-containing solid media and incubated for growth. A colony was picked, used as inoculum for INH-containing TAB, and incubated under growth conditions. When visible growth was apparent, the medium  
10 was used to inoculate liquid TAB media containing INH, and the inoculated medium was allowed to incubate under growth conditions. Aliquots of the culture were then grown again in liquid TAB media containing increased differing concentrations of INH, and cloning of a colony from a  
15 strain that had luxuriant growth in the highest concentration of INH was repeated. This selection procedure was repeated and a series of clones of M. bovis with increasing resistance to isoniazid were obtained. The last strain selected, G4/100, was resistant to 100  $\mu\text{g/ml}$  of  
20 INH.

### Example 2

#### Isolation of INH-resistant Clones from a Cosmid Library prepared from an INH-Resistant Strain

25 A cosmid library from strain G4/100 was prepared in the shuttle vector pYUB18. Plasmid pYUB18 is a multicopy E. coli-mycobacteria shuttle cosmid that contains a selectable kanamycin gene and a cos site (J.T. Beslile et al., J. Bacteriol. 173, 6991 (1991); S.B. Snapper et al.,  
30 Mol. Microbiol. 4:1911 (1990); W.R. Jacobs et al., Methods Enzymol. 204:537 (1991)). A restriction enzyme map of pYUB18 showing some significant features of the genome is shown in Figure 13.

35 The cosmid library was prepared as follows using standard techniques. Chromosomal DNA was purified from

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G4/100, and subjected to partial digestion with Sau3A1; fragments between about 30-50 kb were purified by sucrose gradient purification and ligated to linearized pYUB18. Resulting cosmids were packaged into  $\lambda$ -phage using a commercial kit (Gigapack Gold Stratagene) according to the manufacturer's directions, and transfected into E. coli; approximately 5000 colonies were obtained. The colonies were pooled and the plasmids amplified, using standard plasmid preparation techniques.

10 The cosmid library was then transformed into M. smegmatis strain mc<sup>2</sup> 155 by electroporation. Transformants were selected by growth on medium containing kanamycin. Approximately 1200 kanamycin resistant clones were patched onto media containing INH. Four INH resistant clones were identified.

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### Example 3

#### Isolation and Sequencing of pS5

In order to obtain a plasmid containing mycobacterial genetic material that conferred INH-resistance, the plasmids were extracted from the transformants. Cultures of M. smegmatis (5ml) were incubated with cycloserine and ampicillin for 3 hours before harvest. The cells were pelleted and resuspended in 0.25 ml of 40 mM Tris acetate, 2 mM EDTA, pH 7.9. To this, 0.5 ml of lysing solution was added (50 mM Tris, 3% sodium dodecylsulfate (SDS)) and the solution was mixed for 30 minutes. The sample was heated to 60°C for 20 minutes, cooled for 10 minutes and the DNA was extracted by adding 0.8 ml of phenol (containing 50 mM NaCl). This was centrifuged and the upper layer containing the DNA was removed. To precipitate the DNA, a half volume of 7.5 M ammonium acetate was added, incubated on ice for 30 minutes and then centrifuged for 30 minutes. The DNA was resuspended in 10 mM Tris, 1 mM EDTA.

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The smallest plasmid obtained which conferred an Inh-resistance phenotype on M. smegmatis was 2.3 kb in size and was designated pS5.

The sequence of pS5 was obtained as follows. pS5 was cloned into the vector pBluescript II KS+ (Stratagene, California). This vector contains the T3 and T7 promoters which were used for the sequencing. Sequencing was carried out using the dsDNA cycle sequencing system from GIBCO BRL, Life Technologies, according to the manufacturer's directions. The radioactive labelled nucleotide was either [ $\gamma$ -<sup>32</sup>P] ATP or [ $\gamma$ -<sup>33</sup>P] ATP, available from Amersham. The sequencing program used was GCG, Sequence analysis software package. The nucleic acid sequence for pS5 and the amino acid sequence from two large open reading frames encompassed within it are shown in Figure 9. Figure 10 presents the amino acid sequence of a fragment encoded by nucleic acid residues 1256-2062 (the InhA gene) of the pS5 operon. Figure 11 presents the amino sequence of a fragment encoded by nucleic acid residues 494-1234 of the pS5 operon. Figure 12 presents the nucleic acid sequence of the pS5 M. bovis NZ operon.

#### Example 4

##### Determination of Catalase Activity in an INH-Resistant Strain

Catalase activity of an INH-sensitive strain of M. bovis was determined. The enzyme was first isolated from the strain by pelleting a culture of M. bovis, resuspending it in 50 mM potassium phosphate buffer, pH 7, and adding it to a tube containing 0.5 g zirconium beads (Biospecs products), and vortexing for 5 min. The sample was centrifuged briefly, the supernatant collected and diluted to 4 ml with 50 mM potassium phosphate buffer, and filter sterilized through 0.22  $\mu$ m filters.

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Catalase catalyzes the conversion of  $\text{H}_2\text{O}_2$  to  $\text{H}_2\text{O}$  and  $\text{O}_2$ . Catalase activity was assayed by incubating an aliquot of supernatant, prepared as above, with 3  $\mu\text{M}$   $\text{H}_2\text{O}_2$  in a total volume of 3 ml for 5 minutes. The reaction was  
5 stopped by adding 1.5 ml of titanium tetrachloride reagent (1.5 mg/ml  $\text{TiCl}_4$  in 4.5 M  $\text{H}_2\text{SO}_4$ ). The absorbance was read at 410 nm and the catalase activity was calculated using a standard curve of the amount of hydrogen peroxide versus wavelength at 410 nm; the activity was expressed as  
10  $\mu\text{mol}/\text{min}/\text{mg}$  protein.

Catalase activity of G4/100, G4 and another virulent M. bovis strain were also determined using the above-described procedure. The G4 strain and other virulent M. bovis strains contained similar levels of  
15 catalase activity. Catalase activity was not detected in the G4/100 strain.

To demonstrate that the development of INH-resistance in G4/100 was not due entirely to loss of catalase activity, the plasmid pS5 was electroporated into  
20 G5 to produce G4(S5). G4(S5) grew on media containing a level of INH that prevented growth of G4. Using the method described above, catalase activity was tested in both G4 and G4(S5). G4(S5) which is INH-resistant, and G4 which is INH-sensitive, both showed similar levels of catalase  
25 activity.

#### Example 5

##### Identification of the InhA Gene of M. smegmatis

A spontaneous INH-ETH-resistant mutant of M. smegmatis, mc<sup>2</sup>651, was isolated from wt M. smegmatis in a  
30 single step with a mutational frequency of  $10^{-7}$ . A genomic library from mc<sup>2</sup>651 was constructed in a multicopy (5 to 10 copies) shuttle cosmid vector; the vector was described by  
35 Y. Zhang et al., Mol. Microbiol. 8, 521 (1993). Upon transfer of the library into wt M. smegmatis strains,



cosmid clones were identified that consistently conferred INH-ETH resistance. These results are shown in the table in Figure 1.

Cells of M. smegmatis mc<sup>2</sup>155 bearing the indicated plasmids (derived from insertion into pYUB18) were grown in 7H9 broth containing kanamycin (15µg/ml), and dilutions were plated on 7H10 agar plates containing kanamycin alone or kanamycin with various concentrations of INH or ETH. The strains without any plasmid were grown in 7H9 broth, and dilutions were plated on 7H10 agar plates and on 7H10 agar plates with various concentrations of INH or ETH.

The transformation of cosmids containing a cross-hybridizing DNA fragment from wt (INH-ETH-sensitive strains) of M. smegmatis, M. tuberculosis, M. bovis, M. bovis BCG, and M. avium yielded clones that conferred INH-ETH resistance. The INH-ETH resistance conferred by the transfer of the wt DNA fragment could be due to overexpression of the target, as is the case for the resistance phenotype seen with several antibiotics.

A 3-kb Bam HI DNA fragment from the M. smegmatis cosmid pYUB286 that conferred INH resistance was used as a probe for Southern (DNA) analysis. This probe strongly hybridized to all of the 11 different mycobacterial species tested, including the pathogenic strains M. tuberculosis, M. bovis, M. avium, and M. leprae, demonstrating that this sequence is highly conserved among the mycobacteria.

The DNA fragments hybridizable with those that conferred resistance to INH were isolated from the wt (INH-sensitive) strains of M. smegmatis, M. bovis, and M. tuberculosis, as well as from the INH-resistant mutants of M. smegmatis and M. bovis. Sequence analysis revealed that each strain contains two open reading frames (ORFs), one encoding a 29-kD protein followed by another encoding a 32-kD protein. Figure 2 presents the DNA sequences of INH-

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resistant polynucleotides from M. tuberculosis, M. bovis, and M. smegmatis. The point mutation that differs between the INH-resistant and INH-sensitive M. smegmatis strains, and that determines resistance, is shown in the Figure.

5 Subcloning studies to determine the smallest fragments to confer INH-resistance were performed; the strategy is shown in Figure 3. In the Figure, panel A is subcloning of M. smegmatis mc<sup>2</sup><sub>155</sub>, and panel B is of M. tuberculosis H37Rv. The M. smegmatis mc<sup>2</sup><sub>155</sub> were  
10 transformed with a pool of E. coli-mycobacteria shuttle cosmids, and individual clones were scored for resistance (r,+) or sensitivity (-) to INH and ETH. The ORF preceding inhA is labeled orf1 and the sequence of the intervening DNA is shown. The ribosome binding sites are indicated in  
15 boldface letters. The following enzymes were used for subcloning: B, Bam HI; P, Pst I; S, Spe I, V, Pvu II, N, Nla III; G, Bgl II, H, Nhe I. All the subclones were tested in both orientations. Subcloning analysis of M. bovis DNA yielded results similar to those obtained with M. tuberculosis. Plasmid pYUB291 was also shown to confer INH  
20 and ETH resistance in M. bovis BCG host.

The subcloning studies demonstrated that the second ORF from M. smegmatis was sufficient to confer the INH-resistance phenotype. This second ORF was thus named  
25 the inhA gene. In contrast to the M. smegmatis gene, the M. tuberculosis and M. bovis inhA genes appear to be in an operon with the gene encoding the 29-kD ORF, an observation confirmed by subcloning. In M. tuberculosis and M. bovis DNA, the noncoding region between the two ORFs was  
30 substantially shorter than that in M. smegmatis and may lack a promoter that appears to be present in the latter strain. The inhA DNA sequences have been submitted to GenBank. The accession numbers are U02530 (for M. smegmatis) and U02492 (for M. tuberculosis). The M. bovis  
35 sequence is identical to that of M. tuberculosis.

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The InhA protein may use nicotinamide or flavin nucleotides as substrates or cofactors, as translation of the putative protein encoded therein indicates that it has a putative binding site for these molecules.

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#### Example 6

##### Effect of InhA on Mycolic Acid Biosynthesis

As shown in Figure 4, the predicted InhA proteins of M. tuberculosis, M. bovis, and M. smegmatis show strong  
10 sequence similarity (about 40% identity over 203 amino acids) to the EnvM proteins of S. typhimurium and E. coli. The figure aligns the amino acid sequences of InhA proteins from the indicated strains with the EnvM proteins from E. coli and S. typhimurium. The amino acid sequences were  
15 obtained by conceptual translation of the inhA and envM ORFs. Over a stretch of 203 amino acids, InhA and EnvM show about 75% sequence similarity (40% identity). InhA is highly conserved among mycobacterial strains. The InhA proteins of M. tuberculosis H37Rv and M. bovis are  
20 identical and hence are represented by a single sequence. The M. tuberculosis-M. bovis InhA has greater than 95% identity with the M. smegmatis InhA. The various envM gene products are also highly conserved (98% identity) (F. Turnowsky et al., J. Bacteriol. 171, 6555 (1989); H. Bergler et al., J. Gen. Microbiol. 138, 2093 (1992)). The  
25 protein EnvM is thought to be involved in fatty acid biosynthesis. The relatively close homologies suggest that inhA may be involved in lipid biosynthesis.

The effect of inhA on mycolic acid biosynthesis  
30 was determined in cell-free assays. The M. smegmatis mc<sup>2</sup>155 gene was transformed with pYUB18 vector (strain mc<sup>2</sup>144) or pYUB18 carrying the inhA genes of M. smegmatis (pYUB291, product of subcloning of pYUB286, strain mc<sup>2</sup>801),  
35 M. avium (pYUB317, strain mc<sup>2</sup>832), or M. bovis BCG (pYUB316, strain mc<sup>2</sup>799). Cell-free extracts were prepared

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from each of these strains and from the spontaneous INH-resistant mutant (mc<sup>2</sup>651 of *M. smegmatis*. Incorporation of [1-<sup>14</sup>C]acetate into mycolic acids was measured using an assay described in L.M. Lopez-Marin et al., Biochim. Biophys. Acta 1086, 22 (1991), after preincubation with or without Inh. Protein concentrations in cell-free extracts were adjusted to 0.37 to 0.50 mg/ml, which resulted in the linear incorporation of radioactivity into the mycolic acids after a 1-hour incubation of the cell-free extract with the radioactive acetate. Each assay was done in duplicate, and the experimental error between different experiments was no more than 15%. The results of the cell-free assays of mycolic acid biosynthesis are shown in Figure 5. The INH concentration necessary for strong inhibition of mycolic acid biosynthesis in cell-free extracts of the sensitive strain was about 20 times greater than the MIC (here, 20 x MIC = 100 µg/ml, solid bars.) Open bars, 0 µg/ml; crosshatched bars, 250 µg/ml. A 20- to 50- fold accumulation of INH has been reported to occur inside the mycobacteria.

As seen from the results in Figure 5, compared to wt extracts, cell-free extracts from the resistant mutant mc<sup>2</sup>651 or from resistant merodiploids containing multiple copies of *inhA* showed marked resistance to the INH-mediated inhibition of mycolic acid biosynthesis. This result is supportive of the suggestion that InhA is required for mycolic acid biosynthesis.

#### Example 7

##### Allele Exchange of inhA Genes Conferring Inh-Resistance and Sensitivity Phenotypes

The InhA protein from the INH-resistant mutant (mc<sup>2</sup>651) differs from the wt (mc<sup>2</sup>155) by a single substitution of Ser to Ala at position 94. To test whether this difference caused the INH resistance phenotype in

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mc<sup>2</sup><sub>651</sub>, an allele exchange was performed on the M. smegmatis chromosome. The mc<sup>2</sup><sub>651</sub> cells were transformed with a 45 kb M. smegmatis DNA fragment that contained the wt inhA gene linked to a kan<sup>r</sup> marker gene.

5           A 45 kb long DNA fragment containing the inhA allele from mc<sup>2</sup><sub>155</sub> was cloned into a vector with Pac I sites flanking the insert, and a Tn5seq1 transposon (containing the kan<sup>r</sup> gene) was introduced near inhA. The linear Pac I fragment containing inhA linked to kan<sup>r</sup> was  
10 transformed into mc<sup>2</sup><sub>651</sub> by electroporation. The transformants were plated on 7H10 plates containing kanamycin (15 mg/ml). The kanamycin-resistant transformants were then scored for INH sensitivity on 7H10 plates containing both kanamycin (15 µg/ml) and INH  
15 (10 µg/ml). INH sensitivity contrasformed with kanamycin resistance in 93 of 130 (72%) transformants tested. The remaining transformants were as resistant to INH as was mc<sup>2</sup><sub>651</sub> (MIC = 50 µg/ml). Figure 6 presents a diagram of the allelic exchange experiment.

20           Allelic exchange was confirmed by restriction fragment length polymorphism analysis of the inhA polymerase chain reaction (PCR) products obtained from the recombinants and by Southern blots.

          This result provides evidence that the mutation  
25 of Ser to Ala<sup>94</sup> mediates the INH-resistance phenotype in M. smegmatis.

          An allelic exchange could not be performed in M. bovis because a homologous recombination system is lacking. However, the mutant M. bovis gene conferred a higher level  
30 of resistance to INH (100% survival in 20 µg/ml of INH, MIC = 30 µg/ml) than did the wt M. bovis gene (0% survival in 20 µg/ml of INH, MIC = 15 µg/ml) when transformed into M. smegmatis mc<sup>2</sup><sub>155</sub> on a pYUB18 cosmid vector. These results  
35 shown in the table in Figure 1, demonstrate that the identical mutation of Ser to Ala caused INH resistance in

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M. bovis NZ.Example 8Susceptibility of M. tuberculosis5                   in a Clinical Sample to INH:Single Strand Polymorphism Conformation Analysis

A polynucleotide encoding InhA can be used to assess the susceptibility of various strains of M. tuberculosis in a clinical sample to INH.

10                   The chromosomal DNA of M. tuberculosis is isolated from a clinical sample. Oligonucleotides are prepared using the wild-type inhA sequence of M. tuberculosis. This sequence is depicted in Figure 8. Regions of the inhA gene of M. tuberculosis from the  
15                   clinical sample which are identified by use of the oligonucleotides are amplified using polymerase chain reaction (PCR) to obtain double stranded DNA. Next, in order to determine whether a mutant inhA gene exists, single strand conformation polymorphism analysis is  
20                   performed. An example of single strand conformation polymorphism analysis is described by Telenti et al. in "Detection of Rifampicin-Resistance Mutations in Mycobacterium Tuberculosis", Vol. 341 pages 647-650 (March 1993).

25                   In order to perform single strand conformation polymorphism, PCR is performed after substitution of half of the dCTP by <sup>32</sup>P- $\alpha$ -dCTP or chemiluminescent substrates per reaction to generate a labelled 157 bp product. After amplification, the PCR product is diluted to an appropriate  
30                   concentration with dilution buffer. An aliquot of diluted product is mixed with an appropriate aliquot of sequence loading buffer (Sequenase kit), heated for ten minutes at about 94°C, cooled on ice and loaded onto a non-denaturing  
35                   sequencing format 0.5% MDE gel (Hydrolink, AT Biochem, Malvern, Penn.) Electrophoresis is then performed at room

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temperature and constant power overnight. The gels are then dried and exposed for autoradiography overnight.

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## Claims

1. An isolated wild-type gene which encodes an enzyme which is the target of action for isoniazid.

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2. An isolated wild-type gene which encodes a polypeptide (InhA) which is the target of action for isoniazid (INH).

10

3. A wild-type gene according to claim 2, wherein the gene is selected from the group consisting of that in M. tuberculosis, M. avium, M. smegmatis, and M. bovis.

15

4. An isolated mutant gene that encodes InhA wherein the mutant gene is associated with INH-resistance.

5. An isolated polynucleotide encoding an InhA polypeptide or fragment or variant thereof.

20

6. A polynucleotide according to claim 5, wherein the polynucleotide is a recombinant expression vector comprised of control sequences operably linked to a segment encoding the InhA polypeptide of fragment or variant thereof.

25

7. A host cell comprised of a polynucleotide selected from the group of polynucleotides according to claim 2, or claim 3, or claim 4, or claim 5, or claim 6.

30

8. A method of treating an individual for infection caused by a member of the mycobacterial complex comprising:

35

(a) providing a composition comprised of a polynucleotide capable of inhibiting mRNA activity from an



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inhA operon of the infecting species and a suitable excipient; and

(b) administering a pharmacologically effective amount of said composition to the individual.

5

9. The method of claim 6 wherein the mode of administration of the polynucleotides is selected from oral, enteral, subcutaneous, intraperitoneal and intravenous.

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10. A method of assessing susceptibility of a strain of mycobacteria in a biological sample to INH comprising:

(a) providing the mycobacterial DNA from the biological sample;

15

(b) amplifying a region of the inhA operon;

(c) determining whether a mutation exists within the inhA operon from the biological sample, the presence of the mutation indicating that said mycobacterial strain is resistant to INH.

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11. The method of claim 10 wherein the amplification is by a polymerase chain reaction (PCR).

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12. The method of claim 11 further comprised of providing a comparable portion of wild-type INH-sensitive inhA operon from the mycobacteria, and the determination of whether a mutation exists in the biological sample is by comparison with the wild-type inhA operon.

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13. The method of claim 12, wherein determining whether a mutation exists is performed by single strand conformation polymorphism analysis.

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14. A method of determining whether a drug is

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effective against mycobacterial infection comprising:

- (a) providing isolated InhA;
- (b) providing a candidate drug;
- (c) mixing InhA with substrates for mycolic acid biosynthesis in the presence or absence of the candidate drug; and
- (d) measuring the inhibition of biosynthesis of mycolic acid caused by the presence of the drug, if any.

10           15.    A method of producing a tuberculosis-specific mycolic acid comprising adding purified InhA to substrates required for the biosynthesis of mycolic acid.

15           16.    A method for producing a compound that inhibits InhA activity comprising:

- a. providing purified InhA;
- b. determining the molecular structure of said InhA;
- c. creating a compound with a similar molecular structure to INH; and
- d. determining that said compound inhibits the biochemical activity of InhA.

25           17.    An isolated InhA polypeptide or fragment or variant thereof.

30           18.    A recombinant mycobacterial vaccine comprised of attenuated mutants selected from the group consisting of BCG, M. tuberculosis, and M. bovis, wherein the mutants are host cells containing a mutated inhA gene.

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FIGURE 1

PLASMID	DESCRIPTION	SOURCE OF INSERT	MIC ( $\mu\text{g/ml}$ )	
			INH	ETH
pYUB18	Vector		5	20
pYUB314	pYUB18 :: <i>inhA</i>	<i>M. smegmatis</i> , mc <sup>2</sup> 155	60	>80
pYUB286	pYUB18 :: <i>inhA</i>	<i>M. smegmatis</i> , mc <sup>2</sup> 651	60	>80
pYUB315	pYUB18 :: <i>inhA</i>	<i>M. tuberculosis</i>	15	>30
pYUB316	pYUB18 :: <i>inhA</i>	<i>M. bovis</i> BCG	15	>30
pYUB370	pYUB18 :: <i>inhA</i>	<i>M. bovis</i>	20	>30
pYUB317	pYUB18 :: <i>inhA</i>	<i>M. avium</i>	60	>80



FIGURE 3

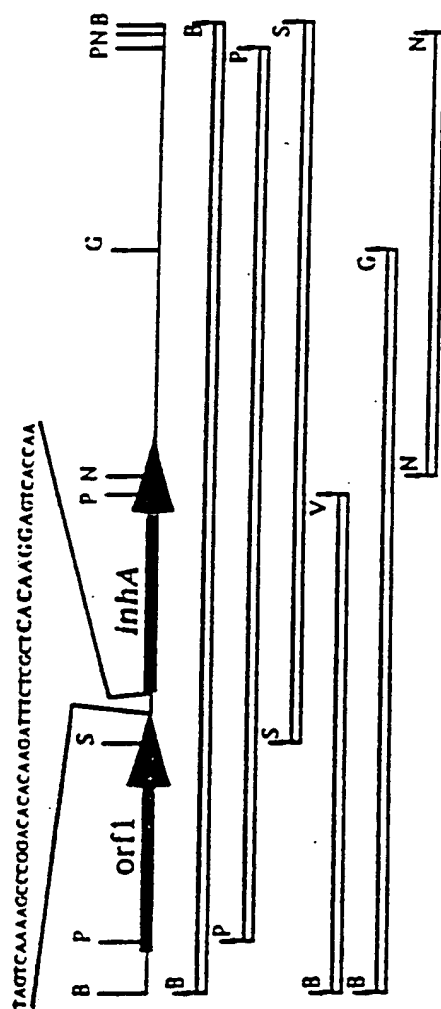
*M. smegmatis*,  
mc<sup>2</sup>155

*M. bovis*,  
BCG

INH<sup>r</sup> ETH<sup>r</sup> INH<sup>r</sup>

PLASMIDS

pYUB18



pYUB291

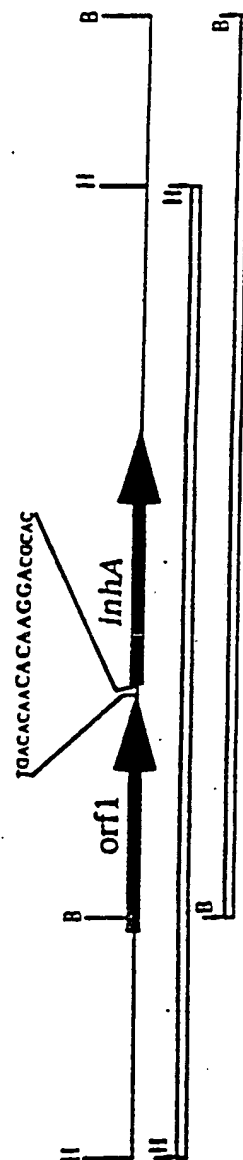
pYUB371

pYUB372

pYUB373

pYUB374

pYUB375



pYUB376

pYUB377

B=BamHI, P=PstI, S=SpeI, V=PvuII, G=BglI, N=NlaIII, H=HheI

+

ND

ND

ND

ND

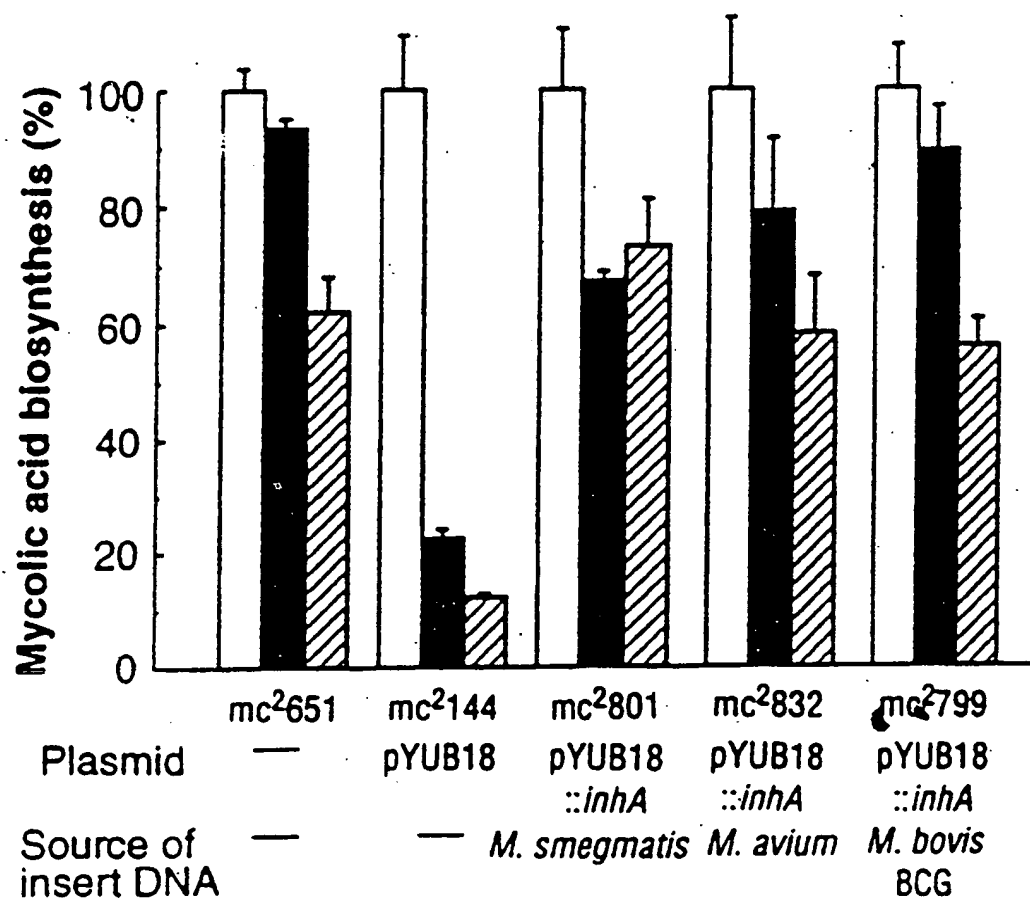
ND

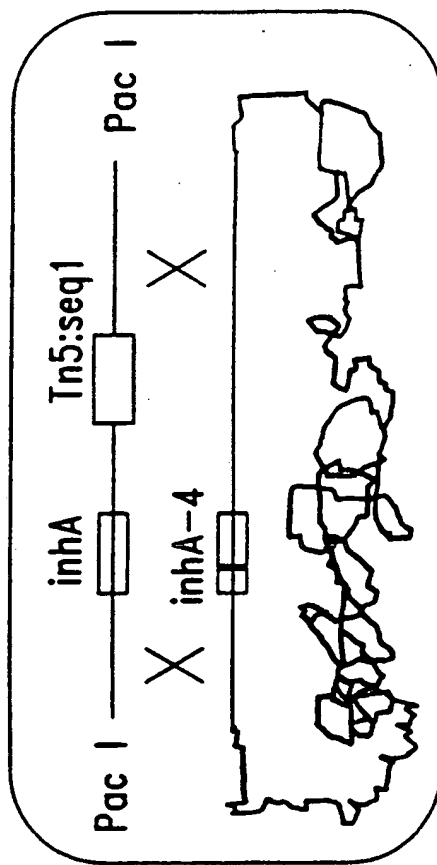
ND

ND

ND



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FIGURE 5



mc<sup>2</sup>651

No. Transformants		Frequency of Cotransformation of	
Kan <sup>r</sup>	Kan <sup>r</sup> lnh <sup>s</sup>	Kan <sup>r</sup>	with INH <sup>s</sup>
28	19		0.68

FIG. 6



# SEQUENCE OF M. SMEGMATIS inhA GENE

1	GGATCGCCG CCTAGCGGC	CACGGGGAGC GTGCCCCTCG	CCCGAGGCCA GGGCTCCGCT	TTTCGGCIG AAAGACCGAC	GACGGGCCAA CTGCCCCGTT	CACGTTAAGT GTGCAATTCA
61	TGACGGGCGA ACTGCCCGCT	AGACGCAGGA TCTGCGTCTT	CGCGAGGAAC GCGCTCCITG	AGAGGATGAC TCICCTACTG	TGTGACTGAC ACACTGACTG	AATCCGGCCG TTAGGCCGGC
121	ACACCGCGGG TGTGGCGCCC	CGAGGCCACT GCTCCGGTGA	GCAGGCCGCC CGTCCGGCGG	CGGCGTTCGT GCCGCAAGCA	CTCCCGTTCC GAGGCAAGC	GTGCTGGTGA CAGGACCACT
181	CCGGTGGTAA GGCCACCAAT	CCGCGGCATC GGCGCCGCTAG	GGCTGGCGA CCGGACCGCT	TGCGCGGACG AGCGCGCTGC	GCTGGCCGCC CGACCGGCGG	GACGGGCACA CTGCCCCGTG
241	AGTGGCCGT TCCACCGGCA	CACCCACCGC GTGGTGCGG	GGTCCGGTG CCAAGGCCAC	CACCCGACGA GTGGGCTGCT	CCTGTTCCGT GGACAAGCCA	GTTCAATGTG CAAGTTACAC
301	ACGTCACCGA TGCAGTGGCT	CAGCGCTGGT GTCGCGACCA	GTCGACCGCG CAGCTGGCGC	CCTTCAAAGA GGAAGTTTCT	GGTCGAGGAG CCAGCTCCTC	CACCAGGGCC GTGGTCCCGG
361	CGGTCGAGGT GCCAGCTCCA	GCTGGTGGCC CGACCACCGG	AACGCAGGCA TTGCGTCCGT	TCTCCAAGGA AGAGGTTCTT	CGCATTCCTC GCGTAAGGAG	ATGGGCATGA TACGCGTACT
421	CCGAGGAGCG GGCTCCTCGC	GTTCTGAAGAG CAAGCTTCCT	GTCATCAACA CAGTAGTTGT	CCAACCTCAC GGTTGGAGTG	GGGCGCGTTC CCCCGCCAAG	CGGTGCGCCC GCCACGCGGG

## FIG. 7A-2

481	ACCGGGCGTC	GGCACCACATG	CAGCGCAAGC	GGTTCGGGCG	CATCATCTTC	ATCGGGTICGG
	TGCGCCGCAG	CGCGTGGTAC	GTCGCGTTCC	CCAAGCCCGC	GTAGTAGAAG	TAGCCAGGCC
541	TCTCGGGCAI	GIGGGGATC	GGCAATCAGG	CCAACIACGC	GGCCGCCAAG	GCGGGCCTGA
	AGAGCCCGTA	CACCCCTAG	CCGTTAGTCC	GGTTGATGCG	CCGGCGGTTC	CGCCCGGACT
601	TCGGCATGGC	CCGCTCGATC	TCCCGTGAGC	TGGACAAGGC	GGCGTCAAC	GCGAACGTGT
	AGCCGTACCG	GGCGAGCTAG	AGGCACTCG	ACCIGTCCG	CCCGCAGTGG	CGCTTGCACA
661	TGCCCCCCCG	TTACATCGAC	ACCGAGATGA	CCCGGGCGCT	CGACGAGCGC	ATCCAGGGGG
	ACGGGGGGCC	AATGAGCTG	TGGCTCTACT	GGGCCCGCGA	GCTGCTCCCG	TAGGTCCCCC
721	GCGCGATCGA	CTTCATCCCG	GACAAGCGGG	TCGGCACGGT	CGAGGAGGTC	GCGGGCGCGG
	CGCGCTAGCT	GAAGTAGGGC	CTGTCGCCC	AGCCGTGCCA	GCTCCTCCAG	CGCCCGCGCC
781	TCAGCTTCCT	GGCCTCGGAG	GACGCTCTCT	ACATCGCGGG	CGCGTCAATC	CCCCTCGACG
	AGTCGAAGGA	CCGGAGCCTC	CTCGGAGGA	TGTAGCGCCC	GCGCCAGTAG	GGGCAGCTGC
841	GCGGTATGGG	CATGGGCCAC	TAGTCAAAAG	CCCGGACACA	CAAGATTCT	CGCTCACAAG
	CGCCATACCC	GTACCCGGTG	ATCAGTTTTC	GGGCCTGTGT	GTTCTAAAGA	GCGAGTGTTC
901	GAGTCACCAA	ATGACAGGCC	TACTCGAAGG	CAAGCGCATC	CTCGTCACGG	GGATCATCAC
	CTCAGTGGTT	TACTGTCTTG	ATGAGCTTCC	GTTCCGCTAG	GAGCAGTCCC	CCTAGTAGTG
961	CGATTCTGTC	AICCGTICC	ACATCGCCAA	GGTCGCCCCAG	GAGGCCGGCG	CCGAACCTGGT
	GCTAAGCAGC	TAGCGCAAGG	TGTAGCGGTT	CCAGCGGGTC	CTCCGGCCAC	GGCTTGACCA
1021	GCTGACCCGT	TTGACCCGCC	TGAAGTTGGT	CAAGCGCATC	GCCGACCGCC	TGCCCCAAGCC
	CGACTGGCCA	AAGCTGGCGG	ACTTCAACCA	GTTCCGGTAG	CGGCTGGCGG	ACGGGTTCGG

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FIG. 7B-1

1081	GGCCCCGCTG	CTGGAACCTG	ACGTGCAGAA	CGAGGAGCAC	CTGTGACATC	TGGCCGACCG
	CCGGGGCGGAC	GACCTTGAGC	TGCACGCTTT	GCTCCTCGTG	GACAGCTGAG	ACCGGCTGGC
1141	GATCACCGCC	GAGATCGGTG	AGGGCAACAA	GATCGACGGT	GTGGTGCACG	CGATCGGGTT
	CTAGTGGCGG	CTCTAGCCAC	TCCCGTTGTT	CTAGCTGCCA	CACCACGTGC	GCTAGCCCAA
1201	CATGCCGCAG	AGCGGTATGG	GCATCAACCC	GTCTTCGAC	CCGCCGTIACG	AGGATGTGTC
	GTACGGCGTC	TCGCCATACC	CGTAGTTGGG	CAAGAAGCTG	CCCGGCAIGC	TCCTACACAG
1261	CAAGGGCATC	CACATCTCGG	CGIACICGTA	CGCCTCGCTC	GCCAAAGCCG	TTCGCCCCAT
	GTCCCGTAG	GTGTAGAGCC	GCA TGAGCAT	GCGGAGCGAG	CGGTTTCGGC	AAGACGGCTA
1321	CATGAATCCG	GGCGGGGGCA	TCGTCGGCAT	GGACTTCGAC	CCCACGGCGG	CGATGCCGGC
	GTACTTAGGC	CCGCCACCAT	AGCAGCCAIA	CCTGAAGCTG	GGGTGCGCGC	GCTACGGCCG
1381	CTACAACTGG	ATGACCGTGG	CCAAGAGCGC	GCTCGAATCG	GTCAACCCGT	TCGTGCGCGG
	GATGTTGACC	TACTGCCAGC	GGTTCICTCG	CGAGCTTAGC	CAGTTGGCCA	AGCAGCGCGC
1441	TGAGGCGGGC	AAGGTGGGGC	TGGCTCGAA	TCTCGTTGGG	GCAGGACCGA	TCCGCACGCT
	ACTCCGCCCCG	TCCACCCCG	ACGGGAGCTT	AGAGCAACGC	CGTCCCTGGCT	AGCGGTGCGA

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## FIG. 7B-2

1501	GGCGATGAGC	GCAATCGTGG	GCGGTGGCT	GGCGACGAG	GCCGGCCAGC	AGATGCAGCT
	CCGCTACTCG	CGTTAGCACC	CGCCACGGGA	CCCGCTGCTC	CGGCCGGTGG	TCTACGTCGA
1561	GCTCGAAGAG	GGCTGGGATC	AGCGCGCGCC	GCTGGGCTGG	AACATGAAGG	ACCCGACGCC
	CGAGCTTCTC	CCGACCCCTAG	TCGCGCGCGG	CGACCCGACC	TTGTACTTCC	TGGGCTGCGG
1621	CGTCGCCAAG	ACCGTGTGG	CACTGCTGTC	GGACTGGCTG	CCGGCCACCA	CCGGCACCGT
	GCAGCGGTTC	TGGCACAGCG	GTGACGACAG	CCTGACCGAC	GGCCGGTGGT	GGCCGTGGCA
1681	GATCTACGCC	GACGGCGGG	CCAGCACGCA	GCTGTGTGGA	TACCGCCGTG	TCGTATGACG
	CTAGATGCGG	CTGCCGCGCG	GGTCGTGGT	CGACAACACT	ATGGCGGCAC	AGCATACTGC
1741	CCTTGCTACT	GCIGTCGTC	GACGGGCGGG	AATCCCCGAG	CAGGTGATGC	CGTCTTGGA
	GGAACGATGA	CGACAGCAAG	CTGCCCGGGC	TTGAGGGCTC	GTCCACIACG	GCAAGAACCT
1801	GAACTCACCA	GGGGCCGGG	AATCCCCAGG	GAGCGGCTGG	AATCGGTGGC	CGAGCACTAT
	CTTGAGTGGT	CCCCCGCGCC	TTAGGGGTCC	CTCGCCGACC	TTAGCCACCG	GCTCTGGATA
1861	CTGCACCTCG	GCGGGGTGTC	ACCGATCAAC	GGCATCAACC	GGGACCTGAT	CGTCGGGATC
	GACGTGAAGC	CGCCCCACAG	TGGCTAGTTG	CGIAGTTGG	CCCTGGACIA	GCAGCGCTAG
1921	GAGCCCGAAC	TCGCCCGACG	CGGCCGCAAC	CTTCCGGTCT	ACTTCGGCAA	CCGCAACTGG
	CTCCGGCTTG	AGCGGGCTGC	GCCGGCGTTG	GAAGGCCAGA	TGAAGCCGTT	GGCGTTGACC
1981	GAGCCGTACG	TCGAAGACAC	TGTCAAGGCG	ATGTCGACA	ACGGAATCCG	TCGTGCGGCG
	CTCGGCATGC	AGCTTCTGTG	ACAGTCCGC	TACAGGCTGT	TGCCTTAGGC	AGCACGCCGC

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2041	GTGTTCCGA	CCTCGGCGTG	GGTGGGTAC	TCGGGATGCG	CCCAGTACCA	GGAGGACATC
	CACAAGCGCT	GGAGCGGCAC	CCCACCCATG	AGCCCTACGC	GGGTCAIGGT	CCTCCTGTAG
2101	GCGCGTGGCC	GGGCCCGCCGC	CGGGCCCCGAG	GCGCCGGAGC	TGGTCAAGCT	GCGCCAGTAT
	CGCGCACCGG	CCCGCGGCGG	GCCCCGGCTC	GCGGGCCCTCG	ACCAGTTCCA	CGCGGTGATA
2161	TCGACCACC	CGCTGTTCGT	CGAGATGTC	GCCGACGCCG	TCGCCGACGC	GCGGGCCACC
	AAGCTGGTGG	GCGACAAGCA	GCCTACAAAG	CGCTGCCGCC	AGCGGCTGCG	GCGCCGGTGG
2221	CTGCCCCGAGG	AACTGCCGGA	CGAAGCGCGG	CTGGTGTTC	CCGCCCCACTC	CATCCCCGCTG
	GACGGGCTCC	TGACGCCCCCT	GCCTCGCGCC	GACCACAAGT	GGCGGGTGAG	GAGGGGGAC

FIG. 7B-3

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## FIG. 7C-1

2281	CGTGCCTGGT	CGCGTTCCGG	TGCAGATCTC	TACGAGCGGC	AGGTGGTTA	CGCCGCGCGG
	GCACGGCGCA	GCGCAACGCC	ACGTCTAGAG	ATGCTCGCCG	TCCACCCCAAT	GCGGCGCGCC
2341	CTGGTCGGG	CCGCAGCCGG	GTACCGCGAA	TACGACCAGG	TATGGCAGTC	CCGGTCCGGC
	GACCAGCGCC	GCGCTCGGCC	CA TGCGGCTT	ATGCTGTCTC	ATACCGTCAG	GGCCAGGCGC
2401	CCGCCGCAGG	TGCCGTGGCT	CGAACCCGAC	GTCCGAGATC	ACCTTGAGGC	GTGGCGCGCC
	GGCGGCGTCC	ACGGCACCGA	GC TTGGGCTG	CAGCCTCTAG	TGGA ACTCCG	CAACCGCGCG
2461	AACGGCACCA	GGCGGTGCAT	CGTGTGTCCC	CTCGGCTTCG	TCGCCGACCA	CATCGAGGTG
	TTGCCGTGGT	CCCGCCAGTA	GCACACAGGG	GAGCCGAAGC	AGCGGCTGGT	GIAGCTCCAC
2521	GTGTGGGATC	TGGACAACGA	ACTGGCCGAG	CAGGCCGCGC	AGGCAGGCAAT	CGCGTTCGCG
	CACACCCTAG	ACCTGTTGCT	TGACCGGCTC	GTCCGGCGGC	TCCGTCCGTA	GCGCAAGCGC
2581	CGTGGCGCCA	CGCCCAACTC	CCAGCCACGT	TTTGCCCAAC	TTGTCTCGA	CCTGATCGAC
	GCACGGCGGT	GCGGGTTGAG	GGTCCGTGCA	AAACGGGTTG	AACAGCAGCT	GGACTAGCTG
2641	GAATGCTGC	ACGGACTTCC	GCCACGCCCG	GTCCAGGGGC	CCGATCCGTG	CCCGCCTACG
	CTTTACGACG	TGCCTGAAGG	CGGTGCGGCC	CAGTCCCCCG	GGCTAGGCAC	GGGCGGATGC
2701	GCAGCAGTGT	CAACGGCGCA	CCGTGCACGC	CGGCCCTGCTC	GGCGTGACCC	GCCCCGGGCG
	CGTCGTACAC	GTGCGCGCGT	GGCACGTGCG	GCCGGACGAG	CCGC ACTGGG	CGGGGCCCCG

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2761	CAGCGAGTCG	GGCCGGGGCGA	GCAAGAACGC	CAGCGGGAAT	GCAGGATCGC	CTCGAGTGGC
	GTGCTCAGC	CCGGCCCGCT	AGTCTTGGC	GTCCGCCCTTA	CGTCCTAGCG	GAGCTCAGCG
2821	GCCATACGGC	CCGAGCGCAC	CACCCGCGTG	AGGGGGCGCA	GGCCCGAGTC	GGCGATCTGA
	CGGTATGCGC	GGCTCGCGTG	GTGGGGGCAC	TCCCCCGCGT	CGCGGCTCAG	CCGCTAGACT
2881	ACCTCCGAGC	AACCTGCGAG	ACCGCTCGGG	ATCAGACCCG	CACTCACCGC	GATGATGGCG
	TGGAGGCTGC	TTGAGACGTC	TGGCGAGCCC	TAGTCTGGGC	GTGAGTGGCG	CTACTACCGC
2941	TCGACATGGG	CGGCGTTCTC	CAGCACCCGC	ACAGCCCCGGG	TCGGCGCGTG	GTCCGGGGACG
	AGCTGTACCC	GGCGCAAGAG	GTGTTGGCG	TGTCGGGCCC	AGCCGGGCAC	CAGCCCCTGC
3001	CGGTGCGCGC	GGCCGGGGCGC	GAGGATCTGC	TCGACCATCC	CGCGCGGATC	C
	GCCACGGGCG	CGGGCCGCGC	CTCCTAGACG	AGCTGGTAGG	GGCGGCCTAG	G

FIG. 7C-2

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## FIG. 8A-1

## SEQUENCE OF THE M. TUBERCULOSIS inhA GENE

1	AGCGCGACAT	ACCTGCTGGG	CAATTCGTAG	GGGTCAATA	CACCCGCAGC	CAGGGCCTCG
	TCGGCGCTGTA	TGGACGACGC	GTTAAGCATC	CCGCAGTTAT	GTGGCGGTG	GTCCCGGAGC
61	CTGCCCAGAA	AGGGATCCGT	CATGGTCGAA	GTGTCTGAG	TCACACCCGAC	AAACGTCACG
	GACGGGTCTT	TCCCTAGGCA	GTACCAGCTT	CACACGACTC	AGTGTGGCTG	TTTGCAGTGC
121	AGCGTAACCC	CAGTCCGAAA	GTCCCCGCCG	GAATCCGAG	CCACGTTACG	CTCGTGGACA
	TGTGGCGCCC	GCTCCGGTGA	CGTCCGGCGG	CGGCGTTCTG	GAGGGCAAGC	CACGACCACT
181	TCGCATTGGG	GGCCCGGCCG	CGGCGAGACG	ATAGTTGTC	GGGTGACTIG	CCACAGCCAC
	ATGGCTAAG	CCGGGCCGGC	CCCGCTCTGC	TATCCAACAG	CCCCACTGAC	GGTGTGGTIG
241	TGAAGGGGCC	AAACCCCCAT	TCGTATCCCG	TTACGICCTG	GTTACCCGAG	GAAACCGGGG
	ACTTCCCCGG	TTTGGGGTA	AGCATAGGGC	AAGTCAGGAC	CAATGGCCTC	CITTTGGCCCC
301	GATCGGGCTG	GCGATCGCAC	ACGGGCTGGC	TGCCGACGGC	CACAAGGTGG	CCGTACCCCA
	CTAGCCCCGAC	CGCTAGCGTG	TCCCGGACCG	ACGGCTGCCG	GTGTTCCACC	GGCAGTGGGT
361	CCGTGGATCC	GGAGCGCCAA	AGGGGCTGTT	TGGCCTCGAA	TGTGACGTCA	CCGACAGCGA
	GGCACCTAGG	CCTCGCGGTT	TCCCCGACAA	ACCGCAGCTT	ACACTGCAGT	GGCTGTGCTT
421	CGCCGTCGAT	CGCGCCTTCA	CGGCGGTAGA	AGAGCACCAG	GGTCCGGTGG	AGGTGCTGGT
	GCGGCAGCTA	GCGCGGAAGT	GCCGCCAICT	TCCTGTGGTC	CCAGGCCAGC	TCCACGACCA



## FIG. 8A-2

481	GTCCAACGCC CAGGTGCGG	GGCCTATCCG CCGGATAGGC	CGGACGCAAT GCCTGCGTAA	CCTCATGCGG GGAGTACGCC	ATGACCGAGG TACTGGCTCC	AAAAGTTCGA TTTTCAAGCT
541	GAAGGTCATC CAGGTGCGG	AACGCCAACC CCGGATAGGC	TCACCGGGGC GCCTGCGTAA	GTTCCGGGTG GGAGTACGCC	ATGACCGAGG TACTGGCTCC	AAAAGTTCGA TTTTCAAGCT
601	CATGCAGCGC CAGGTGCGG	GGCCTATCCG CCGGATAGGC	CGGACGCAAT GCCTGCGTAA	CCTCATGCGG GGAGTACGCC	ATGACCGAGG TACTGGCTCC	AAAAGTTCGA TTTTCAAGCT
661	CATCGGCAAC GIAGCCGTG	CAGGCCAACT GTCCGGTTGA	ACGCAGCCTC TGCCTCGGAG	CAAGGCCGGA GTTCCGGCCT	GTGATTGGCA CACIAACCGT	TGGCCCGCTC ACCGGGCGAG
721	GATCGCCCGC CTAGCGGGCG	GAGCTGTGGA CTCGACAGCT	ACGCAGCCTC TCCGTTTGCA	CAAGGCCGGA CTGGCGCTTA	GTGATTGGCA CACCACCGGG	CGGGCTACAT GCCCCGATGA
781	CGACACCGAT GCTGTGGCTA	ATGACCCCGG TACTGGGCGC	CGCTGGATGA GCGACCTACT	GCGGATTCAG CGCCTAAGTC	GAGGGGCGC GTCCCCCGCG	TGCAATTAT ACGTTAAATA
841	CCCAGCGAAG GGGTGCTTC	ATGACCCCGG GCCCAGCCGT	CGCTGGATGA GGGGCGGGCT	GCGGATTCAG CCAGCGGCCC	CAGGGGGCGC CACCAGTCGA	TCCTGGCTTC AGGACCGAAG
901	CGAGGATGCG GCTCCTACGC	AGCTATATCT TCGATATAGA	CCGGTGGCGT GGCCACGCCA	CAIACCGGTC GTAGGGCCAG	GACGGCGGCA CTGCCGCCGT	TGGGTATGGG ACCCATACCC
961	CCACTGACAC GGTGACTGTG	AACACAAGGA TTGTGTTCTT	CGCACATGAC GCGTGTACTG	AGGACTGCTG TCCTGACGAC	GACGGCAAAC CTGCCGTTTG	GGATTCCTGT CCTAAGACCA
1021	TAGCGGAATC ATCGCCTTAG	ATCACCAGACT TAGTGGCTGA	CGTCGATCGC GCAGCTAGCG	GTTTCACATC CAAAGTGTAG	GCACGGGTAG CGTGCCCATC	CCCAGGAGCA GGTCTCTCGT

## FIG. 8B-1

1081	GGGGCCCCAG	CTGGTGCTCA	CCGGGTTCGA	CCGGCTGCGG	CTGATTCAGC	GCATCACCGA
	CCCGCGGGTC	GACCACGAGT	GGCCCAAGCT	GGCCGACGCC	GACTAAGTCG	CGTAGTGGCT
1141	CCGGCTGCCG	GCAAAGGCCC	CGCTGCTCGA	ACTCGACGTG	CAAAACGAGG	AGCACCTGGC
	GGCCGACGGC	CGTTCCGGG	GGCAGCAGCT	TGACGTGCAC	GTTTTCCTCC	TCGTGGACCG
1201	CAGCTTGCC	GGCCGGGTGA	CCGAGGCGAT	CGGGCCGGGC	AACAAGCTCG	ACGGGGTGGT
	GTCGAACCGG	CCGGCCCACT	GGCTCCGCTA	GCCCCGCCCG	TTGTTGAGC	TGCCCCACCA
1261	GCATTCGATT	GGTTTCATGC	CGCAGACCGG	GATGGGCATC	AACCCGTTCT	TCGACCGCGC
	CGTAAGCTAA	CCCAAGTAGG	GGGTCTGGCC	CTACCCGTAG	TTGGGCAAGA	AGCTGCCGCG
1321	CTACGCGGAT	GTGTCCAAGG	GCAIACCACAT	CTCGGCGTAT	GGCAIAGGACT	TCGACCCCGAG
	GATGCGCCTA	CACAGGTTCC	CGIAGGIGTA	AAGTAGCCAG	CCGIACCCTGA	AGCTGGGCTC
1381	GGCGCTGCTG	CCGATCATGA	ACCCCGGAGG	TTCCATCGTC	GGCATGGACT	TCGACCCCGAG
	CCGCGACGAC	GGCTAGTACT	TGGGGCCTCC	AAGTAGCCAG	CCGIACCCTGA	AGCTGGGCTC
1441	CCGGGCGATG	CCGGCCCTACA	ACTGGATGAC	GGTCGCCAAG	AGCGCGTTGG	AGTCGGTCAA
	GGCCCCGCTAC	GGCCCGGATG	TGACCTACTG	CCAGCGGTTT	TCGGGCAACC	TCAGCCAGTT
1501	CAGGTTCTG	GCGGCGGAGG	CCGGCAAGTA	CGGTGTGCGT	TCGAATCTCG	TTGGCCGACG
	GTCCAAGCAC	CGCGCGCTCC	GGCCGTTTCA	GCCACACGCA	AGCTTAGAGC	AACCGCGTCC

## FIG. 8B-2

1561	CCCTATCCGG	ACGCTGGCGA	TGAGTCCGAT	CGTCGGCGGT	GGCTCGGCG	AAGAGGCCGG
	GGGATAGGCC	TCCGACCGCT	ACTCAGCTA	GCAGCCGCCA	CGCGAGCCGC	TTCTCCGGCC
1621	CGCCCAGATC	CAGCTGCTCG	AGGAGGCGTG	GGATCAGCGC	GCTCCGATCG	GCTGGAACAT
	GGGGCTCTAG	GTCGACGAGC	TCCTCCCGAC	CCTAGTCGG	CGAGGCTAGC	CGACCTTGTA
1681	GAAGGATGCG	ACGCCGGTCC	CCAAGACGGT	GTGCGGCGTG	CTGTCTGACT	GGCTGCCGGC
	CTTCCTACGC	TGCGGCCAGC	GGTTCTGCCA	CACGCGCGAC	GACAGACTGA	CCGACGGCCG
1741	GACCACGGGT	GACATCATCT	ACGCCGACGG	CGGCGCGCAC	ACCCAATTGC	TCTAGAACGC
	CTGGTGCCCA	CTGTAGTAGA	TCCGGCTGCC	GCCGCGCGTG	TGGGTTAACG	AGATCTTGCG
1801	ATGCAATTG	ATGCCGTCTT	GTGCTGTGCG	TTCGGCGGAC	CGGAAGGGCC	CGAGCAGGTG
	TACGTTAAAC	CTGTAGTAGA	TCCGGCTGCC	GCCGCGCGTG	GCCTTCCCGG	GCTCGTCCAC
1861	CGCCCGTTCC	TGGAGAACGT	TACCCGGGGC	CGCGGTGTGC	CTGCCGAACG	GTGGACGGC
	CGGGGCAAGG	ACCTCTTGCA	ATGGGCCCCG	CGGCCACACG	GACGGCTTGC	CAACCTGCGC
1921	GTGGCCGAGC	ACTACCTGCA	TTCCGTGGG	GTATCACCAG	TCAATGGCAT	TAATCGCACA
	CACCGGCTCG	TGATGGACGT	AAAGCCACCC	CATAGTGGCT	AGTTACCGTA	ATTAGCGTGT
1981	CTGATCGCGC	AGCTGGAGGC	GCAGCAAGAA	CTGCCGGTGT	ACTTCGGTAA	CCGCAACTGG
	GACTAGCGCC	TCGACCTCCG	CGTCGTTCTT	GACGGCCACA	TGAAGCCATT	GGCGTTGACC

## FIG. 8B-3

2041	GAGCCGIATG	TAGAAGATGC	CGTTACGGCC	ATGCCGGACA	ACGGTGTCGG	GCGTGCAGCG
	CTCGGCATAC	AICTTCTACG	GCAATGCCGG	IACGGCTGT	TGCCACAGGC	CGCACGTCGC
2101	GTCTTTGCGA	CACTCGCGTG	GAGCGGTTAC	TCGAGCTGCA	CACAGTACGT	GGAGGACATC
	CAGAAACGCT	GTAGACGCAC	CTCGCCAATG	AGCTCGACGT	GTGTCATGCA	CCCTCCTGTAG
2161	GCGCGGCCCC	CCGCGCGGCC	GGCGCGGACG	CGCCTGAACT	GGTAAACTG	CGGCCCTACT
	CGCGCGGGGG	GGCGCGCGGG	CCCGCGCTGC	GCGGACTTGA	CCATTTTGAC	GCCGGGATGA
2221	TCGACCATCC	GCTGTTCTGC	GAGATGTTCC	CCGACGCCAT	CACCGCGGCC	GCCGCAACCG
	AGCTGGTAGG	CGACAAGCAG	CTCTACAAGC	GGCTGCGGTA	GTGGCGCCGG	CGGCGTTGGC

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FIG. 8C-1

2281	TGCGGGGGA	TGCGGGGCTG	GTGTCACCG	CGCATTGAT	CCCGACGGCC	GGCGACCGCC
	ACGCGCCACT	ACGGGCGGAC	CACAAGTGG	GGTAAGCTA	GGGCTGCCGG	CGGCTGGCGG
2341	GCTGTGGCC	CAACCTCTAC	AGCGGCCAAG	TGCGCTACGC	CACAAGGCTG	GTGCGGGCCG
	CGACACCGGG	GTGGAGATG	TGCGGGGTTT	AGCGGATGCG	GTGTTCCGAC	CAGCGCCGGC
2401	CTGCCGGATA	CTGCCGACTT	GACCTGGCCT	GGCAGTCGAG	ATCGGGCCCG	CCGCAGGTGC
	GACGGCCTAT	GACGCTGAAA	CTGGACCGGA	CCGTCAGCTC	TAGCCCCGGC	GGCGTCCACG
2461	GGACCGACCT	GCCAGACGTT	ACCGACCAGC	TCACCGGTCT	GGCTGGGGCC	GGCATCAACG
	GGACCGACCT	CGGCTGCAA	TGGCTGGTGG	AGTGGCCAGA	CCGACCCCGG	CCGTAGTTGC
2521	CGGTGATCGT	GTGTCCCAT	GGATTGCTGG	CCGACCATAT	CGAGGTGGTG	TGGGATCTCG
	GCCACTAGCA	CACAGGGTAA	CCTAAGCAGC	GGCTGGTATA	GCTCCACCAC	ACCCTAGAGC
2581	ACCACGAGTT	GCGATTACAA	GCCGAGGCAG	CGGGCATCGC	GTACGCCCCG	GCCAGCACCC
	TGGTGCTCAA	CGCTAATGTT	CGGCTCCGTC	GCCCCGTAGCG	CAIGCGGGCC	CGGTGCGTGG
2641	CCAATGCCGA	CCCGCGGTTT	GCTCGACTAG	CCAGAGGTTT	GAICGACGAA	CTCCGTTACG
	CGGCATATGG	GGCGGCCAAC	CGAGCTGATC	GGTCTCCAAA	CTAGCTGCTT	GAGGCAATGC
2701	GCCGTATACC	TGCGCGGGTG	AGTGGCCCCG	ATCCGGTGCC	GGGCTGCTCG	TCCAGCAICA
	CGGCATATGG	ACGCGCCCCAC	TCACCGGGGC	TAGGCCACGG	CCCGACAGAC	AGGTCGTAGT

## FIG. 8C-2

2761	ACGGCCAGCC	ATGCCGTCCG	CCGCACIGCG	TGGCTAGCGT	CAGTCCGGCC	AGGCCGAGTG
	TGCCGGTCCG	TACGGCAGGC	GGCGTGACGC	ACCGATCGCA	GTCAGGCCGG	TCCGGCTCAC
2821	CAGGATCGCC	GCACGCTGAG	ACATCCGGGC	CGAGCGCACC	ACGGCGGTCA	ACGGTCTCAA
	GTCCTAGCCG	CACTGGCCGC	TGTAGGCCCG	GCTCGCGTGG	TGCCGCCAGT	TGCCAGAGTT
2881	CGCATCGGTG	GCACGCTGAG	CGTCCGACAA	CGACTGCGTT	CCGATCGGCA	ATCGACTCAG
	GGGTAGCCAC	CGTGCGACTC	GCAGGCTGTT	GCTGACGCAA	GGCTAGCCGT	TAGCTGAGTC
2941	CCCGGCACTG	ACCGCGATGA	TCCCATCGAC	GTGCGCGGCA	TTCTCGAGCA	CCCCCAATGC
	GGGCCGTGAC	TGGCGTACT	AGCGTGCTG	CACGCGCCGT	AAGAGCTCGT	GGCGGTTACG
3001	GGCGGATGGC	GCCTGGTCCG	GAACCCGGTG	TTGCCGTGAC	GATTCCAGCA	ACTGCTCGAC
	CGCGCTACCG	CGCACCAGCC	CTTGGGCCAC	AACGGCACTG	CTAAGCTCGT	TGACGAGCTG
3061	GAGGCCACGG	GGCTTGCCGA	CGTCGCTAGA	TCCCAGTCCG	ATGGTGCCTCA	AGCCTTCGGC
	CTCCGGTGCC	CCGAACCGCT	GCAGCGATCT	AGGGTCAGGC	TACCACGAGT	TCCGAAGCCCG

## AMINO ACID SEQUENCE OF PS5

1 GTTCGCTCCGGCGCGGTCACGCGCATGCCCTCGATGACGCAGATCTCGTCGGGCTCGATG  
-----+-----+-----+-----+-----+-----+  
61 CGCTCTTCCCAGACTTGCAGCCCCGGGGCACGGCGGCGGTTGGTGTGATGATCGCGGCG  
-----+-----+-----+-----+-----+-----+  
121 GGAAGATCCGCGTCGATCCACTTGGCGCCATGGAAGGCAGAAGCCGAGTAGCCGGCCAGC  
-----+-----+-----+-----+-----+-----+  
181 ACGCCGCGGGCGCGAGCGCAGCCACAGCGCTTTTGCACGCAATTGCGCGGTGAGTTCC  
-----+-----+-----+-----+-----+-----+  
241 ACACCCTGCGGCACGTACACGTCTTTATGTAGCGCGACATACCTGCTGCGCAATTCGTAG  
-----+-----+-----+-----+-----+-----+  
301 GCGGTCAATACACCGCAGCCAGGGCCTCGCTGCCCAGAAAGGGATCCGTCATGGTCGAA  
-----+-----+-----+-----+-----+-----+  
361 GTGTGCTGAGTCACACCGACAAACGTCACGAGCGTAACCCAGTGCGAAAGTTCCCGCCG  
-----+-----+-----+-----+-----+-----+  
421 GAAATCGCAGCCACGTTACGCTCGTGGACATACCGATTTGGGCCGGCCGCGGCGAGACG  
-----+-----+-----+-----+-----+-----+  
481 ATAGGTTGTCGGGGTGACTGCCACAGCCACTGAAGGGGCCAAACCCCATTCGTATCCCG  
-----+-----+-----+-----+-----+-----+  
V T A T A T E G A K P P F V S R  
541 TTCAGTCCTGGTTACCGGAGGAAACCGGGGGATCGGGCTGGCGATCGCACAGCGGCTGGC  
-----+-----+-----+-----+-----+-----+  
S V L V T G G N R G I G L A I A Q R L A  
601 TGCCGACGGCCACAAGGTGGCCGTCACCCACCGTGGATCCGGAGCGCCAAAGGGGCTGTT  
-----+-----+-----+-----+-----+-----+  
A D G H K V A V T H R G S G A P K G L F  
661 TGGCGTCGAATGTGACGTCACCGACAGCGACGCCGTCGATCGCGCCTTCACGGCGGTAGA  
-----+-----+-----+-----+-----+-----+  
G V E C D V T D S D A V D R A F T A V E  
721 AGAGCACCAGGGTCCGGTCGAGGTGCTGGTGTCCAACGCCGGCCTATCCGCGGACGCATT  
-----+-----+-----+-----+-----+-----+  
E H Q G P V E V L V S N A G L S A D A F

**FIG. 9A**  
**SUBSTITUTE SHEET (RULE 26)**

781 CCTCATGCGGATGACCGAGGAAAAGTTCGAGAAGGTCATCAACGCCAACCTCACCAGGGGC  
-----+-----+-----+-----+-----+-----+  
L M R M T E E K F E K V I N A N L T G A  
841 GTTCCGGGTGGCTCAACGGGCATCGCGCAGCATGCAGCGCAACAAATTCGGTCGAATGAT  
-----+-----+-----+-----+-----+-----+  
F R V A Q R A S R S M Q R N K F G R M I  
901 ATTCATAGGTTCCGGTCTCCGGCAGCTGGGGCATCGGCAACCAGGCCAACTACGCAGCCTC  
-----+-----+-----+-----+-----+-----+  
F I G S V S G S W G I G N Q A N Y A A S  
961 CAAGGCCGGAGTGATTGGCATGGCCCGCTCGATCGCCCGCAGCTGTGAAGGCAAACGT  
-----+-----+-----+-----+-----+-----+  
K A G V I G M A R S I A R E L S K A N V  
1021 GACCGCGAATGTGGTGGCCCCGGGCTACATCGACACCGATATGACCCGCGCGCTGGATGA  
-----+-----+-----+-----+-----+-----+  
T A N V V A P G Y I D T D M T R A L D E  
1081 GCGGATTCAGCAGGGGGCGCTGCAATTTATCCCAGCGAAGCGGGTCGGCACCCCCGCCGA  
-----+-----+-----+-----+-----+-----+  
R I Q Q G A L Q F I P A K R V G T P A E  
1141 GGTCGCCGGGGTGGTCAGCTTCTGGCTTCGAGGATGCGAGCTATATCTCCGGTGCGGT  
-----+-----+-----+-----+-----+-----+  
V A G V V S F L A S E D A S Y I S G A V  
1201 CATCCCGGTGACGGCGGCATGGGTATGGGCCACTGACACAACACAAGGACGCACATGAC  
-----+-----+-----+-----+-----+-----+  
I P V D G G M G M G H \* M T  
1261 AGGACTGCTGGACGGCAAACGGATTCTGGTTAGCGGAATCATCACCAGACTCGTCGATCGC  
-----+-----+-----+-----+-----+-----+  
G L L D G K R I L V S G I I T D S S I A

FIG. 9B



1321 GTTTCACATCGCACGGGTAGCCCAGGAGCAGGGCGCCCAGCTGGTGCTCACCGGGTTCGA  
-----+-----+-----+-----+-----+-----+-----+  
F H I A R V A Q E Q G A Q L V L T G F D  
1381 CCGGCTGCGGCTGATTACGCGCATCACCGACCGGCTGCCGGCAAAGGCCCGCTGCTCGA  
-----+-----+-----+-----+-----+-----+-----+  
R L R L I Q R I T D R L P A K A P L L E  
1441 ACTCGACGTGCAAAACGAGGAGCACCTGGCCAGCTTGGCCGGCCGGGTGACCGAGGCGAT  
-----+-----+-----+-----+-----+-----+-----+  
L D V Q N E E H L A S L A G R V T E A I  
1501 CGGGGCGGGCAACAAGCTCGACGGGGTGGTGCATGCGATTGGGTTCATGCCGCAGACCGG  
-----+-----+-----+-----+-----+-----+-----+  
G A G N K L D G V V H A I G F M P Q T G  
1561 GATGGGCATCAACCCGTTCTTCGACGCGCCCTACGCGGATGTGTCCAAGGGCATCCACAT  
-----+-----+-----+-----+-----+-----+-----+  
M G I N P F F D A P Y A D V S K G I H I  
1621 CTCGGCGTATTCGTATGCTTCGATGGCCAAGGCGCTGCTGCCGATCATGAACCCCGGAGG  
-----+-----+-----+-----+-----+-----+-----+  
S A Y S Y A S M A K A L L P I M N P G G  
1681 TTCCATCGTCGGCATGGACTTCGACCCGAGCCGGGCGATGCCGGCCTACAACTGGATGAC  
-----+-----+-----+-----+-----+-----+-----+  
S I V G M D F D P S R A M P A Y N W M T  
1741 GGTCGCAAGAGCGCGTTGGAGTCGGTCAACAGGTTCTGTGGCGCGCGAGGCCGGAAGTA  
-----+-----+-----+-----+-----+-----+-----+  
V A K S A L E S V N R F V A R E A G K Y  
1801 CGGTGTGCGTTTGAATCTCGTTGCCGCAGGCCCTATCCGGACGCTGGCGATGAGTGCGAT  
-----+-----+-----+-----+-----+-----+-----+  
G V R S N L V A A G P I R T L A M S A I

FIG. 9C

1861 GCTCGGCGGTGCGCTCGGCGAGGAGGCCGGCGCCCAGATCCAGCTGCTCGAGGAGGGCTG  
-----+-----+-----+-----+-----+-----+  
V G G A L G E E A G A Q I Q L L E E G W  
1921 GGATCAGCGCGWTCCGATCGGCTGGAACATGAAGGATGCOACGCCGGTCGCCAAGACGGT  
-----+-----+-----+-----+-----+-----+  
D Q R A P I G W N M K D A T P V A K T V  
1981 GTGCGCGCTGCTGTCTGACTGGCTGCCGGCGACCACGGGTGACATCATCTACGCCGACGG  
-----+-----+-----+-----+-----+-----+  
C A L L S D W L P A T T G D I I Y A D G  
2041 CGGCGCGCACACCCAATTGCTCTAGAACGCATGCAATTTGATGCCGTCCTGCTGCTGTCG  
-----+-----+-----+-----+-----+-----+  
G A H T Q L L \*  
2101 TTCGGCGGACCGGAAGGGCCCGAGCAGGTGCGGCCGTTCTGGAGAACGTTACCCGGGGC  
-----+-----+-----+-----+-----+-----+  
2161 CGCGGTGTGCCTGCCGAACGGTTGGACGCGGTGGCCGAGCACTACCTGCATTTCGGTGGG  
-----+-----+-----+-----+-----+-----+  
2221 GTATCACCGATC  
-----+-----

FIG. 9D

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## AMINO ACID SEQUENCE OF PS5 ENCODED BY NUCLEIC ACID RESIDUES 1256-2062

MTGLLDGKRI	LYSGIITDSS	IAFHARVAQ	EQGAQLVLTG	FDRRLRIQRI
TDRLPQKAPL	LELDVQNEEH	LASLAGRYTE	AIGAGNKLDG	VVHAIGFMPQ
TGMGINPFFD	APYADVSKGI	HISAYSYSYM	AKALLPIMNP	GGGIVGMDFD
PSRAMPAYNW	MTVAKSALES	VNRFVAREAG	KYGVRSNLVA	AGPIRTLAMS
AIVGGALGEE	AGAQIQLLEE	GWDQRAPIGW	NMKDATPVAK	TVCALLSDWL
PATTGDIYA	DGGAHTQLL			

FIG. 10

## AMINO ACID SEQUENCE OF PS5 ENCODED BY NUCLEIC ACID RESIDUES 494-1234

VTATATEGAK	PPFVSRSVLV	TGNGRGIGLA	IAQRLAADGH	KVAVTHRGSG
APKGLFGVEC	DVTDSDAVDR	AFTAVEEHQG	PVEVLVSNAG	LSADAFLMRM
TEEKFEKVIN	ANLTGAFRVA	QRASRSMQRN	KFGRMIFIGS	VSGSWGIGNQ
ANYAASKAGV	IGMARSIARE	LSKANVTANV	VAPGYIDTDM	TRALDERIQQ
GALQFIPAKR	VGTPAEVAGV	VSFLASEDAS	YISGAVIPVD	GGMGMGH

FIG. 11

DNA Sequence of pS5

```
GTTCGCTCCG GCGCGGTCAC GCGCATGCC TCGATGACGC AGATCTCGTC
51 GGGCTCGATG CGCTCTTCCC AGACTTGCAG CCCCAGGGCA CCGCGGCGGT
101 TGGTGTGAT GATCGCGGCG GGAAGATCCG CGTCGATCCA CTTGGCGCCA
151 TGAAGGCAG AAGCCGAGTA GCCGCCAGC ACGCCGCGC GCGCGGAGCG
201 CAGCCACAGC GCTTTTGCAC GCAATTGCG GGTGAGTTCC ACACCCTGCG
251 GCACGTACAC GTCTTTATGT AGCGCGACAT ACCTGCTGCG CAATTCGTAG
301 GCGTCAATA CACCCGCAGC CAGGGCCTCG CTGCCAGAA AGGGATCCGT
351 CATGGTCGAA GTGTGCTGAG TCACACCGAC AAACGTCACG AGCGTAACCC
401 CAGTGCGGAA GTTCCCGCCG GAAATGCGAG CCACGTTACG CTCGTGGACA
451 TACCGATTTC GGCCCGGCGG CCGCGAGAGC ATAGGTTGTC GGGTGACTG
501 CCACAGCCAC TGAAGGGGCC AAACCCCAT TCGTATCCCG TTCAGTCCCTG
551 GTTACCGGAG GAAACCGGGG GATCGGGCTG GCGATCGCAC AGCGGCTGGC
601 TGCCGACGGC CACAAGGTGG CCGTCACCCA CCGTGGATCC GGAGCGCCAA
651 AGGGGCTGTT TGGCGTCGAA TGTGACGTCA CCGACAGCGA CGCCGTCGAT
701 CGCGCCTTCA CGCGGCTAGA AGAGCACCAG GGTCCGGTCG AGGTGCTGGT
751 GTCCAACGCC GGCCTATCCG CCGACGCATT CCTCATGCGG ATGACCGAGG
801 AAAAGTTCCA GAAGGTCATC ACGCCAACC TCACCGGGC GTTCCGGGTG
851 GCTCAACGGG CATCGCGCAG CATGCAGCGC AACAAATTCTG GTCGAATGAT
901 ATTATAGGT TCGGTCTCCG GCAGCTGGG CATCGGCAAC CAGGCCAACT
```

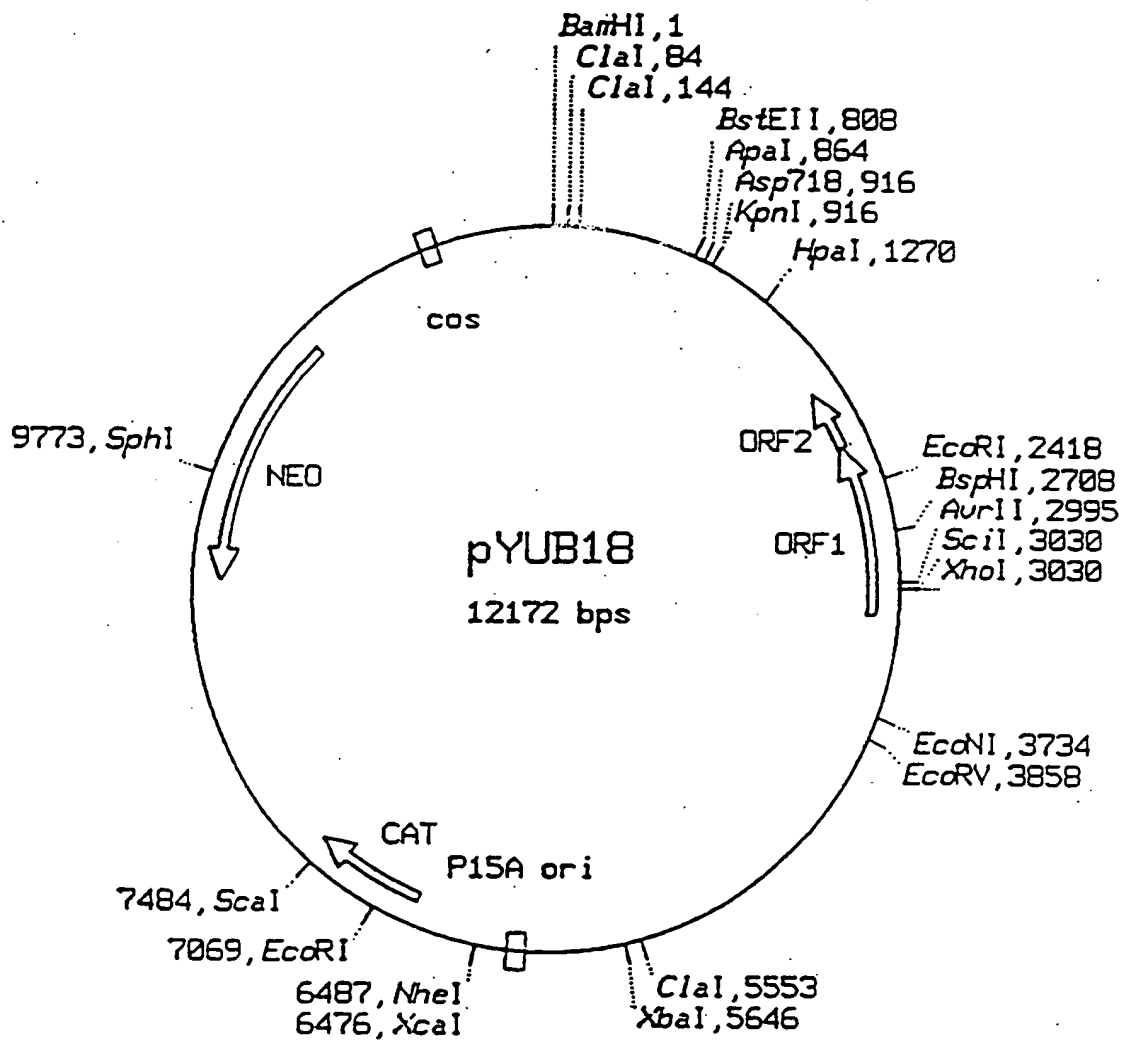
FIG. 12A

951 ACGCAGCCTC CAAGGCCGGA GTGATTGGCA TGGCCCCGCTC GATCGCCCGC  
1001 GAGCTGTGCA AGGCAAACTG GACCGCGAAT GTGGTGGCCC CGGGCTACAT  
1051 CGACACCGAT ATGACCCGCG CGCTGGATGA GCGGATTCAG CAGGGGGCGC  
1101 TGCAATTAT CCCAGCGAAG CCGGTCGGCA CCCCCCGCGG GGTGCGCCGG  
1151 GTGGTCAGCT TCCTGGCTTC CGAGGATGCG AGCTATATCT CCGGTGCGGT  
1201 CATCCCGGTC GACGGCGGCA TGGGTATGGG CCACTGACAC AACACAAGGA  
1251 CGCACATGAC AGGACTGCTG GACGGCAAC GGATTCTGGT TAGCGGAATC  
1301 ATCACCAGCT CGTCGATCGG GTTTCACATC GCACGGGTAG CCCAGGAGCA  
1351 GGGCGCCAG CTGGTGCTCA CCGGGTTCGA CCGGCTGCGG CTGATTCAGC  
1401 GCATCACCGA CCGGCTGCCG GCAAAGGCCC CGCTGCTCGA ACTCGACGTG  
1451 CAAACGAGG AGCACCTGGC CAGCTTGGCC GGCCGGGTGA CCGAGGCGAT  
1501 CCGGGCGGGC AACAACTCG ACGGGTGGT GCATGCGATT GGGTTCATGC  
1551 CGCAGACCGG GATGGGCATC AACCCGTTCT TCGACGCGCC CTACGCGGAT  
1601 GTGTCCAAGG GCATCCACAT CTCGGCGTAT TCGTATGCTT CGATGGCCAA  
1651 GCGGCTGCTG CCGATCATGA ACCCCGAGG TTCCATCGTC GGCATGGACT  
1701 TCGACCCGAG CCGGGCGATG CCGGCCTACA ACTGGATGAC GGTGCGCAAG  
1751 AGCGCGTTGG AGTCGGTCAA CAGGTTCTGT GCGCGCGAGG CCGGCAAGTA  
1801 CCGTGTGCGT TCGAATCTCG TTGCGCGAGG CCCTATCCGG ACGTGGCGA

FIG. 12B

1851 TCAGTGGGAT CGTCGGGGT GCGTCGGCG AGGAGGCCGG CGCCAGATC  
1901 CAGCTGCTCG AGGAGGGCTG GGATCAGCGC GCTCCGATCG GCTGGAACAT  
1951 GAAGGATGCG ACGCCGGTCG CCAAGACGGT GTGCGCGCTG CTGTCTGACT  
2001 GGCTGCCGGC GACCACGGGT GACATCATCT ACGCCGACGG CGGCGCGCAC  
2051 ACCCAATTGC TCTAGAACGC ATGCAATTG ATGCCGTCCT GCTGCTGTG  
2101 TTCGGCGGAC CGGAAGGGCC CGAGCAGGTG CGGCCGTTCC TGGAGAACGT  
2151 TACCCGGGGC CGCGGTGTGC CTGCCGAACG GTTGACGCG GTGGCCGAGC  
2201 ACTACCTGCA TTTCGGTGGG GTATCACCGA TC

FIG. 12C





## INTERNATIONAL SEARCH REPORT

International application No.

T/US94/05344

**A. CLASSIFICATION OF SUBJECT MATTER**

IPC(5) : A61K 48/00; C07H 21/00; C12P 19/34

US CL : 536/23.2; 514/44; 435/91

According to International Patent Classification (IPC) or to both national classification and IPC

**B. FIELDS SEARCHED**

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 536/23.2; 514/44; 435/91

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched  
NoneElectronic data base consulted during the international search (name of data base and, where practicable, search terms used)  
APS, DIALOG**C. DOCUMENTS CONSIDERED TO BE RELEVANT**

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P, X	Science, Volume 263, issued 14 January 1994, A. Banerjee et al., " <i>inhA</i> , a gene encoding a target for isoniazid and ethionamide in <i>Mycobacterium tuberculosis</i> ", pages 227-230, see entire article.	1-7
Y	Chemical Reviews, Volume 90, No. 4, issued June 1990, E. Uhlmann et al., "Antisense oligonucleotides: A new therapeutic principle", pages 543-584, see entire article.	8, 9
Y	Genomics, Volume 5, issued 1989, M. Orita et al., "Rapid and sensitive detection of point mutations and DNA polymorphisms using the polymerase chain reaction", pages 874-879, see entire article.	10-13



Further documents are listed in the continuation of Box C.



See patent family annex.

* Special categories of cited documents:		*T	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
*A	document defining the general state of the art which is not considered to be of particular relevance		
*E	earlier document published on or after the international filing date	*X	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
*L	document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*Y	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
*O	document referring to an oral disclosure, use, exhibition or other means		
*P	document published prior to the international filing date but later than the priority date claimed	*&	document member of the same patent family

Date of the actual completion of the international search

02 AUGUST 1994

Date of mailing of the international search report

19 AUG 1994

Name and mailing address of the ISA/US  
Commissioner of Patents and Trademarks  
Box PCT  
Washington, D.C. 20231

Facsimile No. (703) 305-3230

Authorized officer

Suzanne Ziska, Ph.D.

Telephone No. (703) 308-0196

## INTERNATIONAL SEARCH REPORT

International application No.

PCT/US94/05344

## C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	Journal of Clinical Microbiology, Volume 31, No. 2, issued February 1993, A. Telenti et al., " Rapid identification of Mycobacteria to the species level by polymerase chain reaction and restriction enzyme analysis", pages 175-178, see entire article.	10-13

## INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US94/05344**Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)**

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:  
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

**Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)**

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☒ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:  
1-13
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

☐

The additional search fees were accompanied by the applicant's protest.

☒

No protest accompanied the payment of additional search fees.

**BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING**

This ISA found multiple inventions as follows:

Group I, claims 1-9, claims 1-7 drawn to a first product, a gene, and claims 8 and 9, drawn to a first method of using the first product, a method of treating an individual, classified in Class 536, subclass 23.2, and Class 514, subclass 44, for example.

Group II, claims 10-13, drawn to a second method, a method of assessing susceptibility of a strain of mycobacteria in a biological sample to INH, classified in Class 435, subclass 91, for example.

Group III, claim 14, drawn to a third method, a method of determining whether a drug is effective against mycobacterial infection, classified in Class 437, subclass 7.7, for example.

Group IV, claim 15, drawn to a fourth method, a method for producing a tuberculosis specific mycolic acid comprising adding purified InhA to substrates, classified in Class 435, subclass 41, for example.

Group V, claim 16, drawn to a fifth method, a method for producing a compound that inhibits InhA activity, classified in Class 435, subclass 7.72, for example.

Group VI, claim 17, drawn to a second product, an isolated inhA polypeptide, classified in Class 530, subclass 350, for example.

Group VII, claim 18, a third product, a vaccine, classified in Class 424, subclass 93D, for example.

Each of the products is an independent and distinct product since polypeptides are materially different than nucleic acids (genes) and both are materially different than vaccines. Each of the methods is an independent and distinct method since the methods involve different procedures, the creation of different products. Each grouping of claims forms a separate invention not linked by a special technical feature within the meaning of PCT Rule 13.2 so as to form a single general inventive concept.

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